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(54) Title: NEW PRODUCTS SPECIFIC TO PATHOGENIC STRAINS AND THEIR USE AS VACCINES AND IN IMMUNOTHERAPY

(57) Abstract: The invention relates to isolated antigenic polypeptides obtainable by a process comprising the steps of: 1- selecting on the basis of sequence analysis those of the polypeptides which are either located in the outermembrane or secreted by the bacteria, 2- identifying the genes coding for said polypeptides which are conserved in B2/D clinical isolates, 3- purifying the polypeptides identified in step 1, which are found in step 2 to be conserved in B2/D isolates, 4- testing the polypeptides for immunogenicity using animals models. Application for making vaccines compositions and immunotherapies

New products specific to pathogenic strains and their use as vaccines and in immunotherapy

The invention relates to new products specific to pathogenic strains, particularly to extra-intestinal *E. coli* strains.

It more particularly relates as products to antigenic polypeptides and antibodies directed against said polypeptides and to their use as vaccines and in immunotherapy, respectively.

Although *Escherichia coli* is probably the best known bacterial species and is one of the most common isolated in clinical microbiology laboratories, misconceptions abound regarding the various types of *E. coli* and the infections they cause.

E. coli strains of biological significance to humans can be broadly classified in 3 major groups:

1. Commensal strains, which are part of the normal flora.
2. Intestinal pathogenic strains, which are not part of the normal flora. This group contains various pathotypes (EPEC, EHEC, ETEC, EIEC) not including *Shigella*.
3. Extra-intestinal strains (ExPEC) which are responsible for infections outside the gastro-intestinal (GI) tract, but can also be part of the normal flora. All hosts, either immunocompromised or not are susceptible to these infections.

ExPEC strains are responsible for the majority of the urinary tract infections (UTI) particularly cystitis, pyelonephritis, and cathether associated infections.

They are also responsible for abdominal infections, nosocomial pneumoniae, neonatal meningitidis, soft tissue infections, and bone infections. Each one of these localizations can lead to

bacteremia with a risk of sepsis in case of organ failure. ExPEC strains are indeed the most common Gram negative bacilli isolated from blood cultures.

750 000 cases of bacterial sepsis occur each year in the US, and are responsible for 225 000 deaths. In a recent study on 1690 cases of sepsis, it was shown that the main bacteria species identified is ExPEC (16% of the cases) and then *S.aureus* (14% of the cases).

These numbers demonstrate the importance of ExPEC strains in both hospital and community acquired infections.

ExPEC strains correspond to a homogenous subset of *E. coli* strains. Analysis of phylogenetic relationships among *E. coli* strains by MLEE has revealed that *E. coli* belong to 4 main phylogenetic groups designated A, B1, B2 and D.

The pathogenesis of ExPEC strains is that of extra-cellular microorganisms, i.e., they are well adapted to growth in the extra-cellular fluids and efficiently resist phagocytosis by polymorphonuclear. Initial studies have shown that virulence factors known to be important for the extra-cellular growth are mainly found in B2/D *E. coli*., thus suggesting that B2/D subgroups contain most of the ExPEC strains. This was reinforced by experiments performed on animals showing that B2/D strains are more virulent than A and B1 strains. Subsequent epidemiological studies have indeed confirmed these hypotheses. B2/D isolates are those predominantly responsible for neonatal meningitidis (87%) and community or nosocomial acquired urosepsis, (93 % and 85%, respectively).

Similar results have been reported for cystitis (70% are due to the sole B2 *E. coli*), thus demonstrating that the importance of ExPEC strains.

These recent findings demonstrate that the B2/D subgroup of strains is the *E. coli* core genome the best adapted to growth in extra-cellular fluids.

In addition to this core genome, ExPEC strains have various pathogenicity islands which encode virulence factors associated with the different pathogenesis of extra-intestinal *E. coli* infections (UTI, urosepsis, neonatal meningitidis...). Among the main virulence factors are the capsule, which is well-known to be important for extra-cellular growth, and the iron chelation systems (aerobactin and enterochelin, for example). In addition, depending on the pathogenesis, these strains can produce toxins (CNF, hemolysin...), adhesins (pap, sfa...) and other iron chelation systems.

The notion that B2/D *E. coli* correspond to a distinct subset of pathogenic *E. coli* strains is reinforced by the fact that B2/D *E. coli* are not broadly isolated from the stools of humans. They were recovered from only 11% of individuals, whereas A and B1 subgroups are present in the stools of 74% of the individuals of a human population.

As mentioned above the pathogenesis of ExPEC strains relies on their ability to multiply in the extra-cellular fluids and to resist bactericidal activity of the complement and phagocytosis by polymorphonuclear. Therefore, as for other extra-cellular pathogens (*Haemophilus influenzae*, *Streptococcus pneumonieae* and *Neisseria meningitidis*) a protective antigen against ExPEC has to induce antibodies

that promote opsonisation and/or the bactericidal activity of serum.

Considering the above statements, an efficient antigen has to be largely represented among the population of B2/D *E. coli*. Similarly to other extra-cellular pathogens, the capsular polysaccharide would be an ideal antigen, however most pathogenic B2 strains express the K1 polysaccharide. The latter has a structure identical to that of group B meningococcus, which is non-immunogenic and shares common antigens with the brain. Another possible target may be the lipopolysaccharide (LPS). However there are a large number of different LPS serotypes that are shared by various subgroups.

The inventors have now found that some specific components coded by the B2/D genome, but absent from A and B1 *E. coli* strains, are particularly useful as antigens and can specifically prevent the pathologies due to ExPEC strains. Homologs of these antigenic components can be found in other pathogenic bacterial species and therefore are useful to prevent the pathologies caused by these bacteria. Accordingly, any reference to products specific to ExPEC strains and to their uses will encompass components in these species.

For example homologuous antigens could be present in the following species and be as such used for prevention of disease due to the bacteria:

Pseudomonas aeruginosa, Escherichia coli O157:H7, *Yersinia pestis, Vibrio cholerae, Legionella pneumophila, Salmonella enterica, Salmonella typhimurium, Haemophilus influenzae, Neisseria meningitidis, Neisseria gonorrhoeae, Bacillus anthracis, Burkholderia cepacia, Campylobacter jejuni, Chlamydia pneumoniae, Chlamydia trachomatis,*

Clostridium botulinum, *Clostridium difficile*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Helicobacter pylori*, *Klebsiella pneumoniae*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Pseudomonas aeruginosa*, *Salmonella paratyphi*, *Salmonella typhi*, *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Listeria monocytogenes*, *Moxarella catarrhalis*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*, *Staphylococcus epidermidis*, *Streptococcus pneumoniae*, and any species falling within the genera of any of the above species.

It is then an object of the invention to provide new isolated antigenic polypeptides, and polynucleotides belonging to the core B2/D genome and not present in commensal *E. coli*.

Another object of the invention is to provide antibodies raised against such antigenic polypeptides, or peptidic fragments.

It is still another object of the invention to provide vectors and host cells containing said polynucleotides.

Another object of the invention is to provide vaccine compositions specific to extra intestinal infections caused by ExPEC and pathologies caused by other pathogenic strains expressing antigenic polypeptides homologous to the ExPEC antigenic polypeptides.

The invention also relates to means for detecting and treating a development of *E. coli* in a human or animal compartment which is extra-intestinal (systemic and non-diarrhoeal infections, such as septicaemia, pyelonephritis, or meningitis in the newborn).

The isolated antigenic polypeptides used according to the invention are selected among polypeptides specific to B2/D *E. coli* strains and not present in A and B1 isolates of *E. coli*. They are encoded by genes belonging to the core B2/D genome and are not present in commensal *E. coli*.

They have a sequence selected in the group comprising the sequences of SEQ ID N°11 to N°66 or 133-145 or homologous sequences with a minimum of 25% of identity with the whole sequences SEQ ID N°11 to N°66, or 133-145, respectively.

The isolated polypeptides having SEQ ID N° 14, 15, 17, 21, 22, 23, 28, 29, 30, 32, 36, 38, 39, 41-44, 46, 49, 50, 52 to 55, 58, 60, 63, 133-138 are new polypeptides and therefore are part of the invention.

The invention also relates to homologous isolated antigenic peptides, comprising polypeptides having at least 25% identity to a polypeptide having a sequence SEQ ID N° as above defined, more particularly having SEQ ID N°14, 15, 17, 21, 22, 23, 28, 29, 30, 32, 36, 38, 39, 41-44, 46, 49, 50, 52 to 55, 58, 60, 63, 133-138, or at least 25% identity to a fragment comprising at least 5, at least 10, at least 20, at least 30, at least 40, at least 50, at least 60 or more than 60 consecutive amino acids of a polypeptide having a sequence corresponding to said SEQ ID N°s, as determined using BLASTP or BLASTX with the default parameters.

Said polypeptides are obtainable by a process comprising the steps of :

a- selecting on the basis of sequence analysis those of the polypeptides which are either located in the outermembrane or secreted by the bacteria,

b- identifying the genes coding for said polypeptides which are conserved in B2/D clinical isolates,

c- purifying the polypeptides identified in step a, which are found in step 2 to be conserved in the B2/D isolates,

d- testing the polypeptides for immunogenicity using animals models.

By the term "conserved", it is meant, according to the invention, that the genes coding for the polypeptides are present with a frequency of at least 50% in B2/D isolates, preferably greater than 60%, more preferably greater than 80% and even more preferably greater than 85%, and in less than 40% in A/B isolates, preferably in less than 20%, more preferably in less than 15%.

The animal models used in step c are infected adult animals, eventually immunodepressed.

The adult animals particularly mice, are infected intraperitoneally, the endpoint being the animal death and/or bacteremia measurement.

The animals can be immunodepressed by injection, for example, of cyclophosphamide which induces a neutropenia. Such a model will validate the use of the antigen for prevention of *E. coli* sepsis in immunodepressed patients. Another animal model could be for example 2 to 3 day old infant mice.

The variants or fractionnal sequences conserving the B2/D properties and which are antigenic as defined in step 4 of the above process are also part of the invention. The term "variant" is herein intended to mean any sequence having insertions and/or deletions and/or substitutions with respect

to the parent sequence. The term "fractional" is herein intended to mean any fragment of the parent sequence.

The invention also relates to the use of isolated polynucleotides coding for a polypeptide such as above defined according to the universal genetic code and taking into account the degeneracy of this code. The term "polynucleotide" encompasses any nucleotidic sequence such as DNA, including cDNA, RNA, including mRNA.

Said polynucleotides have preferably sequences corresponding to SEQ ID N°77 to SEQ ID N°132 or 146 to 158 .

More preferably, said polynucleotides have sequences corresponding to SEQ ID N° 80, 81, 83, 87, 88, 89, 94, 95, 96, 98, 102, 104, 105, 107-110, 112, 115, 116, 118, 119, 126, 127, 130, 132, 135, 146-151.

The invention also relates to the homologs to said polynucleotides . Said homologs may have at least 25% identity to a polynucleotide having said sequences, or at least 25% identity to a fragment comprising at least 15, at least 30, at least 60, at least 90, at least 120, at least 150, at least 180 or more than 180 consecutive nucleotide of a polynucleotide having one of said SEQ ID N°s, as determined using BLASTN with the default parameters, and are encompassed by the invention inasmuch as they are capable of coding for a polypeptide having the antigenic properties of those according to the invention.

The present application is also aimed towards any vector comprising at least one of said polynucleotides and also any cell transformed by genetic engineering, characterized in that it comprises, by transfection, at least one of said

polynucleotides and/or at least one vector according to the invention, and/or in that said transformation induces the production by this cell of at least one polypeptide corresponding to a polynucleotide such as above-defined.

The invention also relates to a process for isolating and identifying antigenic polypeptides, therefore useful as vaccine for *E. coli*.

Such a process comprises the steps of

a- selecting on the basis of sequence analysis those of the polypeptides which are either located in the outermembrane or secreted by the bacteria,
b- identifying the genes coding for said polypeptides which are conserved in B2/D clinical isolates,
c- purifying the polypeptides identified in step a, which are found in step 2 to be conserved in B2/D isolates,
d- testing the polypeptides for immunogenicity using animals models.

The selected antigenic polypeptides, alone or in combination, are capable of inducing an antibody response for prevention of infections due to ExPEC strains regardless of the pathogenesis and of the infection site (UTI, pyelonephritis, sepsis, bacteremia, neonatal meningitis).

Such polypeptides particularly have sequences SEQ ID N°1 to SEQ ID N°66, or 133-145 or correspond to homologous sequences.

The invention thus relates to vaccine compositions specific to *E. coli* extra-intestinal infections, comprising an effective amount of at least one antigenic polypeptide or fragment thereof as above defined, with a carrier, particularly at

least one polypeptide of SEQ ID N°1 to SEQ ID N°66, except SEQ ID N°8, and 133-145 and the homologous polypeptides.

Such vaccine compositions are particularly useful for preventing urinary system infections, pyelonephritis, sepsis, bacteremia, neonatal meningitis.

The vaccine compositions of the invention are indicated for :

- immunodepressed patients, ideally before the start of the immunosuppressive therapy : patients suffering from cancer, diabetes, leukaemia, transplant patients, patients receiving long-term steroids therapy.
- Patients before surgery where there is a high risk of *E. coli* infections (abdominal surgery).
- In all these cases, the *E. coli* vaccine of the invention could be administered in association with a *Staphylococcus aureus* vaccine,
- Patients with recurrent UTI, especially after one episode of pyelonephritis.
- The prevention of neonatal infections will require vaccination of the mother, implying vaccination long before pregnancy to avoid potential problem. Ideally such a vaccine should be associated with a Group B *Streptococcus* polysaccharide vaccine in order to also prevent late onset neonatal infections. It should be pointed out that the induction of a level of antibodies against B2/D *E. coli* in pregnant women would also prevent UTI, which are always a risk in the context of a pregnancy.

The formulation and the dose of said vaccine compositions can be developped and adjusted by those skilled in the art as a function of the indication targeted, of the method of

administration desired, and of the patient under consideration (age, weight).

These compositions comprise one or more physiologically inert vehicles, and in particular any excipient suitable for the formulation and/or for the method of administration desired.

For example the vaccine could be a suspension of the purified polypeptide in sterile water with aluminium based miniral salt as adjuvant and be administred subcutanously with a first and boosting injection.

The antibodies raised against the above-identified polypeptides are also part of the invention.

They are capable of binding to said polypeptides in physiological-type conditions (*in vivo* or mimicking *in vivo*) when administered to a human or animal organism, and ELISA-type conditions when said binding product is intended to be used in assays and methods *in vitro*. Such antibodies advantageously inhibit the extra-intestinal growth of ExPEX strains in human or animal.

They are particularly useful for immunotherapy applications with antibodies specific to polypeptidic antigens, for treatment and prevention of severe infections in at risk populations such as neonates or patients undergoing surgical procedures. For these applications specific human monoclonal antibody (Mab) will be derived from the peptides or polypeptides.

The methods for manufacturing such antibodies using the polypeptides according to the invention are available to those skilled in the art. They are conventional methods which

comprise, in particular, the immunization of animals such as rabbits and the harvesting of the serum produced, followed optionally by the purification of the serum obtained. A technique suitable for the production of monoclonal antibodies is that of Köhler and Milstein (Nature 1975, 256:495-497).

Said antibodies do not recognize the cells of the human or animal to which it is intended.

In particular for immunotherapy applications with monoclonal antibodies specific to polypeptidic antigens, for treatment and prevention of severe infections in at risk populations such as neonates or patients undergoing surgical procedures. For these applications specific human monoclonal antibody will be derived from the peptides or polypeptides.

The antibodies or fragments thereof are advantageoulsy humanized when intended for a human administration.

Alternatively, humanized Mab could be derived from murine or rat Mab specific of the antigen. These fully humanized Mab are constructed using conventional molecular techniques to graft complementarity-determining regions from the parent murine or rat antibacterial antibody into human IgG1 kappa heavy and light-chain frameworks.

The present invention is also aimed towards the use, in an effective amount, of at least one of polypeptides having SEQ ID N°14, 15, 17, 21, 22, 23, 28, 29, 30, 32, 36, 38, 39, 41-44, 46, 49, 50, 52 to 55, 58, 60, 63, 133-138, antibodies or polynucleotides for the diagnosis of the presence or absence of undesirable extra-intestinal *E. coli*, and/or for the diagnosis of an extra-intestinal *E. coli* infection.

The detection of the presence or absence of such compounds can in particular be carried out by nucleotide hybridization, by PCR amplification or by detection of their polypeptide products. Detection of the presence of such compounds makes it possible to conclude that a B2/D *E. coli* strain is present.

The invention also relates to pharmaceutical compositions for alleviating and/or preventing and/or treating an undesirable growth of *E. coli* comprising an effective amount of at least one polypeptide as above defined, particularly having SEQ ID N°1-66 to 133-145, in combination with a pharmaceutically acceptable carrier.

Preferred pharmaceutical compositions comprise at least one polypeptide having SEQ ID N°14, 15, 17, 21, 22, 23, 28, 29, 30, 32, 36, 38, 39, 41-44, 46, 49, 50, 52 to 55, 58, 60, 63, 133-138,

The present application is also aimed towards any use of a polypeptide such as above defined for the manufacture of a composition, in particular of a pharmaceutical composition, intended to alleviate and/or to prevent and/or to treat an undesirable growth of *E. coli*, such as an *E. coli* infection, (for example systemic and non-diarrhoeal infections), the presence of extra-intestinal *E. coli* or a sanitary contamination.

The present invention is illustrated by the examples which follow and which are given in a non limiting capacity and with reference to figures 1 and 2, wherein

- Figure 1 represents a protein purification result after cloning and expression, and

- Figure 2 is a picture of the DNA array after hybridization with the genomic DNA from a B2/D reference strain.

Example 1: Assay for the immunogenicity of a selected polypeptide from sequences 1-66 and 133-145 (except SEQ ID N°8)

. Cloning expression and purification of the selected polypeptide.

The nucleic acid having SEQ ID N°95 encoding the polypeptide corresponding to SEQ ID N°28 was cloned without the signal sequence (coding the 16 first amino acids) in a prokaryotic expression vector according to classical methods for cloning. The recombinant plasmid was used to transform the *E. coli* strain BL21. Transformed cells containing the recombinant plasmid were selected in LB medium with 100µg/ml ampicillin. Individual clones are picked and grown in presence of IPTG 1mM to induce recombinant protein expression. Total protein content of the culture cells was extracted by cell lysis. Recombinant protein was purified by affinity columns.

Protein purification after cloning and expression

Total cell lysat of IPTG-induced bacteria were mixed with Ni-NTA matrix (Qiagen®) for 60 min et 4°C and loaded into a column. After washing the column to remove non specific binding, the recombinant protein was eluate 3 times with 1 ml elution buffer pH 5.9. The protein was then eluate 4 times with 1 ml elution buffer pH 4.5.

Figure 1 represents a Coomassie blue stained SDS gel of recombinant protein after affinity column purification: PM:

markers E1-4: sample collected from each purification fraction. Arrow indicate the band corresponding to the recombinant protein.

. Test for immunogenicity in an animal model

Polypeptide preparation from SEQ ID N°28 was injected to Swiss mice to induce an antibody response as follows :

At d0 a first immunisation was done by injecting 20µg of the protein at in 100µg solution of PBS and complet Freund adjuvant (1:1). Control animals were injected with 100µl solution of PBS and complet Freund adjuvant (1:1).

Boosting injection at d21 with 10µg of protein in 100µl PBS and complet Freund adjuvant (1:1).

Sera from vaccinated animals was prepared from blood drawn by puncture in the tail of the mice.

Detection of specific antibodies in animal sera, at d20 before the boosting injection, was performed by western blot according to standart protocol. Purified polypeptide was subjected to electrophoresis (10µg per lane) and transfert to nitrocellulose membrane.

The membranes were then saturated by incubation 35 min with PBS/Tween20 0.1%/powder milk 5%.

Diluted sera was incubated with the membrane for 45 min. Membranes were washed three time 5 min with PBS/tween. Bound antibodies were then recognized by an anti-mouse IgG coupled to horseradish peroxidase enzyme. After washing 3 times with PBS/Tween and 3 time with PBS, enzymatic activity was revealed

by addition of chromogenic substrate DAB and hydrogen peroxyde.

Results : Sera from vaccinated animal, diluted at 1/100 revealed a unique band corresponding to the injected polypeptide. No antibody to the polypeptide could be detected in sera from control animals.

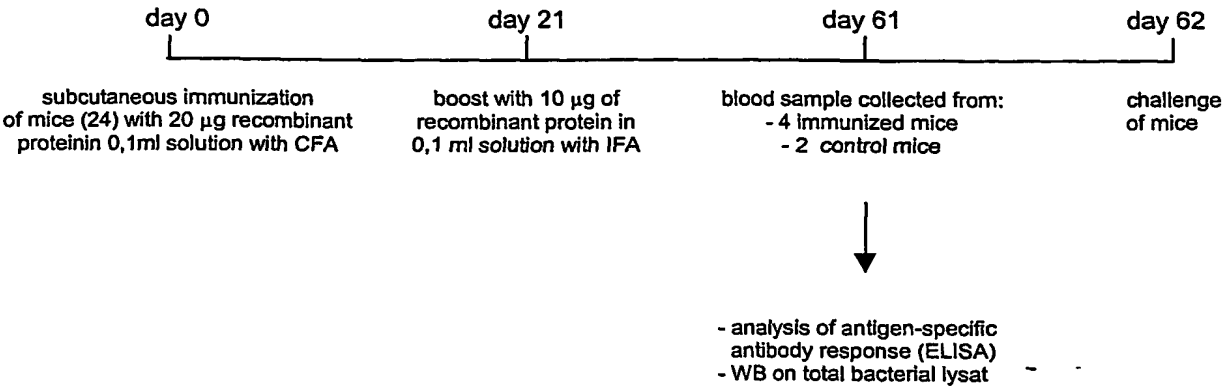
At d42, 300 µl of cyclophosphamide and 200µl at d45 were injected IP in the mice to induce neutropenia in order to increase the susceptibility to the challenge infection.
At d46 vaccinated and control mice were challenged by intraperitoneal injection of the wt B2/D strain C5 of *E. coli* at a dose equal to 10 time the LD50 (letal dose).

Immunogenicity of the selected polypeptide and protection conferred by vaccination with the seleted polypeptide was assessed by the survival of vaccinated animals three days post challenge.

Another example of vaccination to demonstrate immunogenicity of polypeptides:

- 24 Balb/c mice, female, 6 weeks old were immunized by subcutaneous Injection of the protein in Complete Freund's adjuvant, and 14 control mice were injected with CFA and PBS
- 3 weeks later a boost injection of 10 µg of protein in with incomplete Freund's adjuvant.

VACCINATION PROTOCOL



Before challenge at d62, sera was collected at d61 to analyze the antibody response in the vaccinated animals.

- WB analysis of sera from immunized mice were performed to detect the antibody response to the recombinant proteine used for immunization as described above.

- An ELISA assay was set up to measure antibody titer in vaccinated animals:

- Each recombinant protein was coated on a 96-well plates with (200 ng/100 µl coating buffer), plates are saturat with 3%BSA in PBS.
- Twofold serial dilution of sera were made in PBS 1X/1% BSA from 1:500, to 1: 1024000 and incubated on the plate, antiboby binding was reavealed using a rabbit Anti-mouse IgG conjugated with Peroxydase and OPD(o-phenylenediamine) chromogen substrate.
- Read the OD_{495} with Sanofi Diagnostics Pasteur PR2100®

- Results:

Table 1. Sera titer against recombinant protein by ELISA

SEQ ID	serum1	serum 2	serum 3	serum 4	Control	recombinant protein
2	128	64	128	512	<0,5	
140	>64	>64	>64	>64	<0,5	+
31	>64	>64	>64	>64	<0,5	+
49	>64	>64	>64	>64	<0,5	+
51	>64	>64	>64	>64	<0,5	+
25	>64	>64	>64	>64	<0,5	+
7	16	8	>64	<0,5	<0,5	+
19	>64	>64	>64	>64	0,5	+
3	>64	>64	>64	>64	<0,5	+
26	512	128	64	256	<0,5	+
18	>64	>64	>64	>64	0,5	+
32	>64	>64	>64	>64	0,5	+
53	>64	>64	>64	>64	0,5	+
587	>64	16	32	32	<0,5	+
11	>64	32	32	64	<0,5	+
36	512	256	512	256	<0,5	+
10	32	128	256	128	0,5	+
47	512	512	512	512	0,5	+
20	1024	256	256	512	<0,5	+
17	1024	512	128	512	<0,5	+

- To assess the ability of sera to recognize the native antigen expressed by the bacteria, western blot was also performed on whole bacteria lysat.

To this end, bacteria were grown in LB medium supplemented or not with iron chelator until OD600=0.5-0.6 and pelleted by centrifugation 5 minutes at 10000 rpm. The pellet was lysed by resuspension in 1X loading buffer containing SDS and heated 5 min at 95°C before migration on the gel.Western blot assay was then performed with sera from controls and vaccinated animals.

Results in table 2 shows the results obtained with Sera from vaccinated mice against recombinant protein and against *E.coli* lysat.

Table 2: reactivity in Western Blot of sera from mice vaccinated with polypeptides encoded by the different ORFs

SEQ ID N°	whole cell lysate	recombinant protein
2	+	+
140	+	+
26	+	+

- Protection assay, end point: mortality

At d62, 20 vaccinated and 10 control mice were challenged with an *E.coli* virulent strain belonging to B2 group at a dose equal to the LD 50 (5.10^5 cfu/mice) by intraperitoneal injection. Mortality is recorded at 48h, results in Table 3 are expressed as a percentage of protection representing the difference of survival in vaccinated versus control mice goups.

Table 3 : Protection obtained in mice challenged after immunization with proteines encoded by the corresponding ORFs.

SEQ ID N°	% protection
2	52
26	66
36	46
10	30
47	60
20	25

- Protection assay, end point: bacteremia

At d62, 10 vaccinated and 5 control mice were challenged with an Ecoli virulent strain belonging to B2 group at a dose equal to the 1/5 of the LD 50 (1.10^5 cfu/mice) by intraperitoneal

injection.With this infectious dose the mice survived the infection at d48. At 48h blood was collected for each mice in presence of heparin .To assess bacteremia , the blood was plated on LB media and colonies count measured after overnight culture.

Example 2: Distribution of the DNA sequence of ORFs specific for B2/D group of *E.coli* in clinical isolates.

To make a DNA arrays membrane specific for B2/D group of *E.coli* , DNA corresponding to ORFs that were identified as specific for B2/D core genome of *E.coli* was amplified by PCR and spotted on nylon membrane using standard methods to those skilled in the art.

Chromosomal DNA from 30 *E.coli* clinical isolate strains (of which 23 were from pathological conditions and 6 isolated from human normal flora), was prepared and radiolabelled with 33P.

DNA from these clinical isolates was then hybridized to the B2/D specific DNA array, the results were read by a phosphoimager and spots reactivity was analyzed with an image analysis software. If hybridization gave a positive signal for a particular ORF, this ORf is considered to be present in the genome of the isolate. Quality control of the array is the hybridization of a probe DNA from a reference strain of *E.coli* as shown in figure 2, which represents a picture of the DNA array after hybridization with the genomic DNA from a B2/D reference strain.

The details of the method used for these experiments has been described previously in Tinsley et al. Methods Enzymol. 2002, 358; 188-207.

Results presented in Table 4 are expressed as the frequency of each ORF detection in the three different group A, B and D of *E.coli* strains.

Table 4 :Presence of Orfs encoding antigens in *E.coli* clinical isolate genomes

Frequency of positive signal %	Clinical isolate groups		
	A	D	B2
SEQ ID N°	N=6	n=5	n=18
86	17	20	100
119	0	80	100
137	0	0	100
77	0	100	94
78	0	100	100
79	0	100	100
80	0	0	100
84	0	0	100
82	0	0	100
88	0	0	100
83	0	0	94
85	0	0	78
88	0	0	56
81	33	20	100
89	33	60	67
90	0	0	61
91	17	80	67
94	0	0	100
92	0	0	100
93	0	0	100

96	0	100	100
85	17	100	100
97	0	70	100
98	0	0	100
99	0	0	78
101	0	80	100
102	0	0	100
104	0	0	11
103	0	0	100
105	0	0	67
100	0	100	100
111	17	0	61
115	0	0	78
114	0	0	83
113	0	0	94
120	33	80	16
125	17	0	89
109	0	0	33
110	0	0	17
124	0	0	72
126	0	80	78
116	0	0	33
112	0	0	22
106	17	0	33
117	33	80	11
132	33	80	22
122	0	0	22
74	0	0	89
70	0	0	33
73	0	0	89
71	50	100	22
75	0	0	0
76	0	0	56
67	0	0	50

69	100	100	100
68	67	100	100
152	0	0	94
153	0	100	100
150	0	0	11
142	83	100	78
157	67	0	94
156	17	100	100
100	0	100	100
154	0	80	67
147	0	0	100
146	17	100	100
158	17	100	89
107	17	0	78
72	50	100	44
151	0	0	11
149	0	0	28
148	0	0	6

Example 3 : Vaccines compositions intended for prevention of any form of infection by ExPEC.

The polypeptide coded by a sequence comprising SEQ ID N°28 is conjugated with a toxin and added to a physiologically inert vehicle.

This conjugated peptide is optionnally added to a childhood vaccine.

The composition is sterilized and can be injected parenterally, subcutaneously or intramuscularly.

Said composition can also be sprayed onto mucosa with the aid of a spray.

CLAIMS

1.The isolated polypeptides having SEQ ID N° 14, 15, 17, 21, 22, 23, 28, 29, 30, 32, 36, 38, 39, 41-44, 46, 49, 50, 52 to 55, 58, 60, 63, 133-138.

2- Isolated antigenic polypeptides according to claim 1 obtainable by a process comprising the steps of :
a- selecting on the basis of sequence analysis those of the polypeptides which are either located in the outermembrane or secreted by the bacteria,
b- identifying the genes coding for said polypeptides which are conserved in B2/D clinical isolates,
c- purifying the polypeptides identified in step a, which are found in step b to be conserved in B2/D isolates,
d- testing the polypeptides for immunogenicity using animals models.

3. Isolated polynucleotides, coding for a polypeptide according to claim 1 or 2, according to the universal genetic code.

4. Isolated polynucleotides according to claim 3, having sequences selected in the group comprising SEQ ID N° 80, 81, 83, 87-89, 94-96, 98, 102, 104, 105, 107-110, 112, 115, 116, 118, 119, 126, 127, 130, 132, 135, 146-151.

5. An expression vector comprising at least an isolated polynucleotide according to claim 3 or 4.

6. A host cell comprising an expression vector according to claim 5.

7. A process for isolating and identifying antigenic polypeptides, useful as vaccines comprising the steps of :
a- selecting on the basis of sequence analysis those of the polypeptides which are either located in the outermembrane or secreted by the bacteria,
b- identifying the genes coding for said polypeptides which are conserved in B2/D clinical isolates,
c- purifying the polypeptides identified in step a, which are found in step b to be conserved in B2/D isolates,
d- testing the polypeptides for immunogenicity using animals models.

8. The process of claim 7, comprising the use of infected adult animals, eventually immunodepressed, and of infant animals as models for neonatal infections.

9. The use of at least one polypeptide or fragment of these polypeptides selected in the group comprising SEQ ID N°1 to SEQ ID N°66(except SEQ ID N°8), or 133-145 as antigens and the homologous sequences.

10. A vaccine composition specific to *E. coli* extra-intestinal infections, comprising an effective amount of at least one antigenic polypeptide such as selected by the process of claim 7, or according to claim 9, alone or in combination, particularly at least one polypeptide having a sequence selected in the group comprising SEQ ID N°1 to SEQ ID N°66, or 133-145, except SEQ ID N°8 and the homologous sequences, with a carrier.

11. The vaccine composition of claim 10 for preventing urinary system infections, pyelonephritis, sepsis, bacteremia, neonatal meningitidis.

12. The vaccine composition of claim 10 or 11, adapted to specific indication in combination with components directed against other bacteria, such as *S.aureus* or group B *Streptococcus*. Or other bacteria implicated in systemic infections.

13. Antibodies or fragments thereof directed against a polypeptide such as used according to claim 9.

14. Monoclonal antibodies against epitopes of polypeptide and there use as pharmaceutical compound for treatment or prevention of severe infection due to Expec in neonates and patients at risk for such infections.

15. A method for detecting the presence or absence of undesirable extra-intestinal *E. coli*, and/or for the diagnosis of an extra-intestinal *E. coli* infection, comprising the use of at least one polypeptide such as defined in claim 1 or 2 or a polynucleotide according to claim 3 or 4, or an antibody to claim 13 or 14, said polypeptide(s) being optionally in combination with anyone of the polypeptides having SEQ ID N°1-66 to 133-145.

16. Pharmaceutical composition for alleviating and/or preventing and/or treating an undesirable growth of *E. coli* comprising an effective amount of at least one polypeptide according to claim 9, in combination with a pharmaceutically acceptable carrier.

FIGURE 1

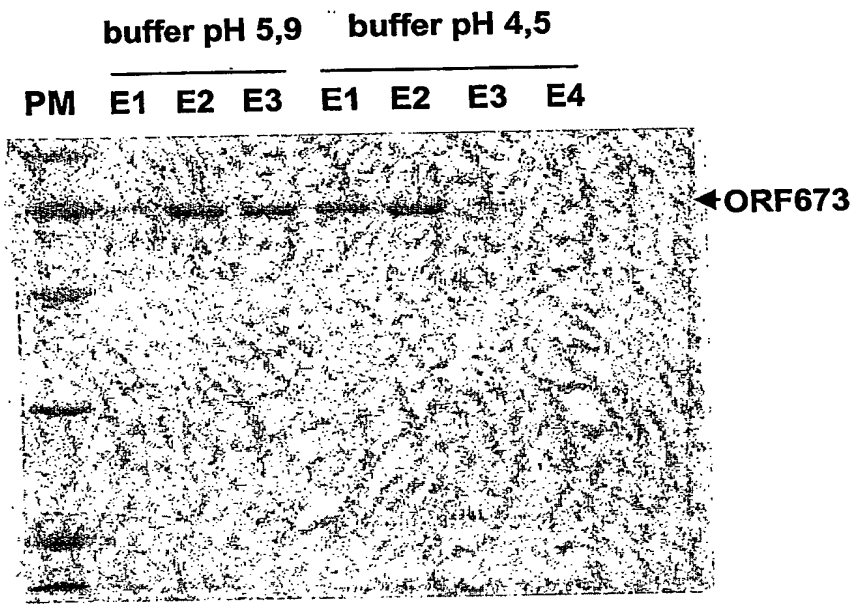
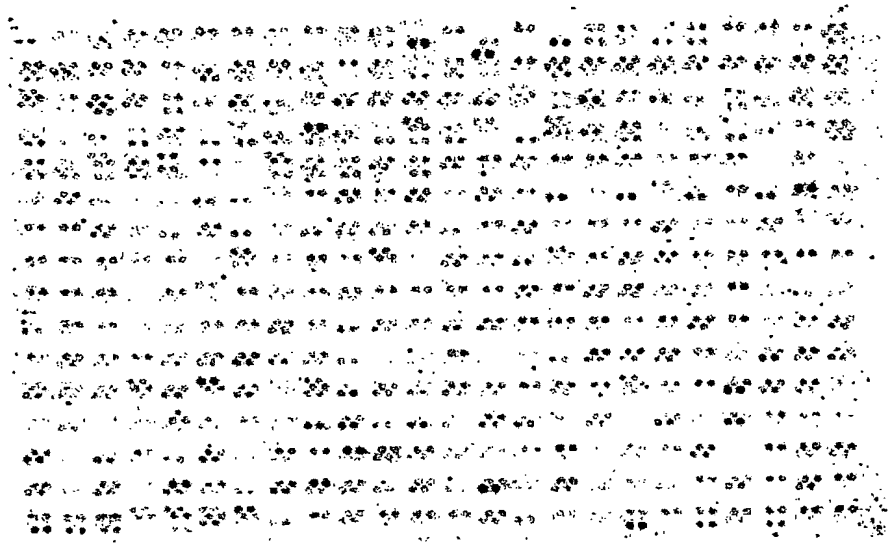


FIGURE 2



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35 40 45

Gly Asn Leu Tyr Val Ser Asp Phe Pro Asn Ala Gly Ser Gly Ser Pro
50 55 60

Trp Val Asn Phe Asp Leu Ser Leu Thr Gly Cys Gln Asn Met Asn Thr
65 70 75 80

Val Arg Ala Thr Phe Ser Gly Thr Ala Asp Gly Gln Thr Tyr Tyr Ala
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Asn Thr Gly Asn Ala Gly Gly Ile Lys Ile Glu Ile Gln Asp Arg Asp
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Gly Ser Asn Ala Ser Tyr His Asn Gly Met Phe Lys Thr Leu Asn Val
115 120 125

Gln Asn Asn Asn Ala Thr Phe Asn Leu Lys Ala Arg Ala Val Ser Lys
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35 40 45

Val Ser Ser Thr Val Val Ser Ala Pro Glu Leu Ser Asp Ala Gly Val
50 55 60

Thr Ala Ser Asp Lys Leu Pro Arg Val Leu Pro Gly Leu Asn Ile Glu
65 70 75 80

Asn Ser Gly Asn Met Leu Phe Ser Thr Ile Ser Leu Arg Gly Val Ser
85 90 95

Ser Ala Gln Asp Phe Tyr Asn Pro Ala Val Thr Leu Tyr Val Asp Gly
100 105 110

Val Pro Gln Leu Ser Thr Asn Thr Ile Gln Ala Leu Thr Asp Val Gln
115 120 125

Ser Val Glu Leu Leu Arg Gly Pro Gln Gly Thr Leu Tyr Gly Lys Ser
130 135 140

Ala Gln Gly Gly Ile Ile Asn Ile Val Thr Gln Gln Pro Asp Ser Thr
145 150 155 160

Pro Arg Gly Tyr Ile Glu Gly Gly Val Ser Ser Arg Asp Ser Tyr Arg
165 170 175

Ser Lys Phe Asn Leu Ser Gly Pro Ile Gln Asp Gly Leu Leu Tyr Gly
180 185 190

Ser Val Thr Leu Leu Arg Gln Val Asp Asp Gly Asp Met Ile Asn Pro
195 200 205

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Val Lys Leu Arg Leu Ala Pro Asp Asp Gln Pro Trp Glu Met Gly Phe
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Ala Ala Ser Arg Glu Cys Thr Arg Ala Thr Gln Asp Ala Tyr Val Gly
                245                 250                 255

Trp Asn Asp Ile Lys Gly Arg Lys Leu Ser Ile Ser Asp Gly Ser Pro
            260                 265                 270

Asp Pro Tyr Met Arg Arg Cys Thr Asp Ser Gln Thr Leu Ser Gly Lys
        275                 280                 285

Tyr Thr Thr Asp Asp Trp Val Phe Asn Leu Ile Ser Ala Trp Gln Gln
    290                 295                 300

Gln His Tyr Ser Arg Thr Phe Pro Ser Gly Ser Leu Ile Val Asn Met
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Ser Gln Arg Trp Asn Gln Asp Val Gln Glu Leu Arg Ala Ala Thr Leu
                325                 330                 335

Gly Asp Ala Arg Thr Val Asp Met Val Phe Gly Leu Tyr Arg Gln Asn
            340                 345                 350

Thr Arg Glu Lys Leu Asn Ser Ala Tyr Asp Met Pro Thr Met Pro Tyr
        355                 360                 365

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    370                 375                 380

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Arg Phe Ser His Asp Lys Ser Ser Thr Gln Tyr His Gly Ser Met Leu
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            420                 425                 430
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Tyr Glu Leu Gly Thr Arg Tyr Glu Thr Ala Asp Val Thr Leu Gln Ala
485 490 495

Ala Thr Phe Tyr Thr His Thr Lys Asp Met Gln Leu Tyr Ser Gly Pro
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Val Gly Met Gln Thr Leu Ser Asn Ala Gly Lys Ala Asp Ala Thr Gly
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Val Glu Leu Glu Ala Lys Trp Arg Phe Ala Pro Gly Trp Ser Trp Asp
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Ile Asn Gly Asn Val Ile Arg Ser Glu Phe Thr Asn Asp Ser Glu Leu
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Tyr His Gly Asn Arg Val Pro Phe Val Pro Arg Tyr Gly Ala Gly Ser
565 570 575

Ser Val Asn Gly Val Ile Asp Thr Arg Tyr Gly Ala Leu Met Pro Arg
580 585 590

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Leu Arg Gln Gly Thr Tyr Ala Thr Leu Asp Ser Ser Leu Gly Trp Gln
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Ser Gly Asp Glu Glu Glu Thr Ser Lys Tyr Lys Gly Gly Asp Asp His
50 55 60

Asp Thr Val Phe Ser Gly Gly Ile Ala Val Gly Tyr Asp Phe Tyr Pro
65 70 75 80

Gln Phe Ser Ile Pro Val Arg Thr Glu Leu Glu Phe Tyr Ala Arg Gly
85 90 95

Lys Ala Asp Ser Lys Tyr Asn Val Asp Lys Asp Ser Trp Ser Gly Gly
100 105 110

Tyr Trp Arg Asp Asp Leu Lys Asn Glu Val Ser Val Asn Thr Leu Met
115 120 125

Leu Asn Ala Tyr Tyr Asp Phe Arg Asn Asp Ser Ala Phe Thr Pro Trp
130 135 140

Val Ser Ala Gly Ile Gly Tyr Ala Arg Ile His Gln Lys Thr Thr Gly
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180 185 190

Val Arg Tyr Asp Val Thr Pro Asp Ile Ala Leu Asp Leu Ser Tyr Arg
195 200 205

Tyr Leu Asp Ala Gly Asp Ser Ser Val Ser Tyr Lys Asp Glu Trp Gly
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35 40 45

Thr Val Val Leu Asp Asn Ala Tyr Thr Ser Asp Leu Ile Ala Ala Asn
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Ser Thr Ser Gln Trp Lys Asn Phe Ser Leu Thr Leu Thr Asn Cys Gln
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Asn Val Asn Asn Val Thr Ser Phe Gly Gly Thr Ala Glu Asn Thr Asn
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Tyr Tyr Arg Asn Thr Gly Asp Ala Thr Asn Ile Met Val Glu Leu Gln
100 105 110

Glu Gln Gly Asn Gly Asn Thr Pro Leu Lys Val Gly Ser Thr Lys Val
115 120 125

Val Thr Val Ser Asn Gly Gln Ala Thr Phe Asn Leu Lys Val Arg Ala
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35 40 45

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Glu Ser Lys Ile Ser Thr Asn Ser Ala Tyr Ser His Asp Leu Leu Ser
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Tyr Lys Asn Asp Lys Thr Phe Arg Asn Leu Glu Ile Phe Gly Asp Ser
                245                 250                 255

Gly Ser Gly Ala Tyr Leu Tyr Asp Asn Lys Leu Glu Lys Trp Val Leu
            260                 265                 270

Val Gly Thr Thr His Gly Ile Ala Ser Val Asn Gly Asp Gln Leu Thr
        275                 280                 285

Trp Ile Thr Lys Tyr Asn Asp Lys Leu Val Ser Glu Leu Lys Asp Thr
    290                 295                 300

Tyr Ser His Lys Ile Asn Leu Asn Gly Asn Asn Val Thr Ile Lys Asn
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Thr Asp Ile Thr Leu His Gln Asn Asn Ala Asp Thr Thr Gly Thr Gln
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Glu Lys Ile Thr Lys Asp Lys Asp Ile Val Phe Thr Asn Gly Gly Asp
            340                 345                 350

Val Leu Phe Lys Asp Asn Leu Asp Phe Gly Ser Gly Gly Ile Ile Phe
        355                 360                 365

Asp Glu Gly His Glu Tyr Asn Ile Asn Gly Gln Gly Phe Thr Phe Lys
    370                 375                 380
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Asn Val Gln Lys Lys Gln Gly Ala Asn Ile Lys Ile Gly Glu Gly Asn
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Val Ile Leu Asn Glu Glu Gly Thr Phe Asn Asn Ile Tyr Leu Ala Ser
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Thr Thr Ile Thr Asn Ser Asp Thr Thr Lys Glu Ala Val Leu Ala Ile
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Asn Ala Ser Leu Thr Met Gln Gly His Ala Thr Glu His Ala Ile Phe
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Arg Ser Ser Ala Asn His Cys Ser Leu Val Phe Leu Cys Gly Thr Asp
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Thr Leu Asn Gly Ala Thr Phe Leu Asp Asn Thr Pro Ile Ser Ile Asp
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Lys Gly Ala Lys Val Ile Ala Gln Asn Ser Met Phe Thr Thr Lys Gly
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Ile Asp Ile Ser Gly Glu Leu Thr Met Met Gly Ile Pro Glu Gln Asn
755 760 765

Ser Lys Thr Val Thr Pro Gly Leu His Tyr Ala Ala Asp Gly Phe Arg
770 775 780

Leu Ser Gly Gly Asn Ala Asn Phe Ile Ala Arg Asn Met Ala Ser Val
785 790 795 800

Thr Gly Asn Ile Tyr Ala Asp Asp Ala Ala Thr Ile Thr Leu Gly Gln
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Pro Glu Thr Glu Thr Pro Thr Ile Ser Ser Ala Tyr Gln Ala Trp Ala
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Glu Thr Leu Leu Tyr Gly Phe Asp Thr Ala Tyr Arg Gly Ala Ile Thr

835 840 845

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850 855 860

Ser Gln Ser Ser Ile Asn Arg Leu Glu Thr Lys Asp Ser Met Val Arg
865 870 875 880

Phe Thr Gly Asp Asn Gly Lys Phe Thr Thr Leu Thr Val Asn Asn Leu
885 890 895

Thr Ile Asp Asp Ser Ala Phe Val Leu Arg Ala Asn Leu Ala Gln Ala
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Asp Gln Leu Val Val Asn Lys Ser Leu Ser Gly Lys Asn Asn Leu Leu
915 920 925

Leu Val Asp Phe Ile Glu Lys Asn Gly Asn Ser Asn Gly Leu Asn Ile
930 935 940

Asp Leu Val Ser Ala Pro Lys Gly Thr Ala Val Asp Val Phe Lys Ala
945 950 955 960

Thr Thr Arg Ser Ile Gly Phe Ser Asp Val Thr Pro Val Ile Glu Gln
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Lys Asn Asp Thr Asp Lys Ala Thr Trp Thr Leu Ile Gly Tyr Lys Ser
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Val Ala Asn Ala Asp Ala Ala Lys Lys Ala Thr Leu Leu Met Ser Gly
995 1000 1005

Gly Tyr Lys Ala Phe Leu Ala Glu Val Asn Asn Leu Asn Lys Arg
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1160 1165 1170

Ser Gly Lys Gln Phe Ser Trp Lys Asp Gln Gly Met Asn Leu Thr
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1190 1195 1200

Asp Val Gly Lys Ser Phe Ser Gly Lys Asp Trp Lys Val Thr Ala
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Arg Ala Gly Leu Gly Tyr Gln Phe Asp Leu Phe Ala Asn Gly Glu
1220 1225 1230

Thr Val Leu Arg Asp Ala Ser Gly Glu Lys Arg Ile Lys Gly Glu
1235 1240 1245

Lys Asp Gly Arg Met Leu Met Asn Val Gly Leu Asn Ala Glu Ile
1250 1255 1260

Arg Asp Asn Leu Arg Phe Gly Leu Glu Phe Glu Lys Ser Ala Phe
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Ser Phe
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Phe Pro His His Gly Asp Asp Gly Arg Asn Ser Ile Glu Pro Ser Ile
50 55 60

Ser Arg Ala Ala His Thr Asp Arg Leu Arg Phe Val Cys Met Thr Arg
65 70 75 80

Thr Gly Ser Thr Thr Ser Arg Pro Phe Cys Pro Ile Pro Arg Ser Pro
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Ala Leu Asn Ala Ser Gly Gln Gln Asp Ser Gly Phe Trp Gly Val Ser
100 105 110

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35 40 45

Val Phe Tyr His Phe Ser Ala Thr Ser Phe Asp Ser Val Asp Gly Thr
50 55 60

Arg His Tyr Arg Val Trp Thr Ala Val Pro Asn Thr Thr Ala Pro Ala
65 70 75 80

Ser Gly Tyr Pro Ile Leu Tyr Met Leu Asp Gly Asn Ala Val Met Asp
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100 105 110

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115 120 125

Ser Arg Ala Tyr Asp Tyr Thr Pro Ala Ala Glu Ser Arg Lys Thr Asp
130 135 140

Leu His Ser Gly Arg Phe Ser Arg Lys Ser Gly Gly Ser Asn Asn Phe
145 150 155 160

Arg Gln Leu Leu Glu Thr Arg Ile Ala Pro Lys Val Glu Gln Gly Leu
165 170 175

Asn Ile Asp Arg Gln Arg Arg Gly Leu Trp Gly His Ser Tyr Gly Gly
180 185 190

Leu Phe Val Leu Asp Ser Trp Leu Ser Ser Ser Tyr Phe Arg Ser Tyr
195 200 205

Tyr Ser Ala Ser Pro Ser Leu Gly Arg Gly Tyr Asp Ala Leu Leu Ser
210 215 220

Arg Val Thr Ala Val Glu Pro Leu Gln Phe Cys Thr Lys His Leu Ala

225 230 235 240

Ile Met Glu Gly Ser Ala Thr Gln Gly Asp Asn Arg Glu Thr His Ala
245 250 255

Val Gly Val Leu Ser Lys Ile His Thr Thr Leu Thr Ile Leu Lys Asp
260 265 270

Lys Gly Val Asn Ala Val Phe Trp Asp Phe Pro Asn Leu Gly His Gly
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Pro Gly Val Ser Val Ile Thr Ser Glu Asp Ile Lys Lys Thr Pro Pro
50 55 60

Val Asn Asp Leu Ser Asp Ile Ile Arg Lys Met Pro Gly Val Asn Leu
65 70 75 80

Thr Gly Asn Ser Ala Ser Gly Thr Arg Gly Asn Asn Arg Gln Ile Asp
85 90 95

Ile Arg Gly Met Gly Pro Glu Asn Thr Leu Ile Leu Ile Asp Gly Val
100 105 110

Pro Val Thr Ser Arg Asn Ser Val Arg Tyr Ser Trp Arg Gly Glu Arg
115 120 125

Asp Thr Arg Gly Asp Thr Asn Trp Val Pro Pro Glu Gln Val Glu Arg
130 135 140

Ile Glu Val Ile Arg Gly Pro Ala Ala Ala Arg Tyr Gly Ser Gly Ala
145 150 155 160

Ala Gly Gly Val Val Asn Ile Ile Thr Lys Arg Pro Thr Asn Asp Trp
165 170 175

His Gly Ser Leu Ser Leu Tyr Thr Asn Gln Pro Glu Ser Ser Glu Glu
180 185 190

Gly Ala Thr Arg Arg Ala Asn Phe Ser Leu Ser Gly Pro Leu Ala Gly
195 200 205

Asp Ala Leu Thr Thr Arg Leu Tyr Gly Asn Leu Asn Lys Thr Asp Ala
210 215 220

Asp Ser Trp Asp Ile Asn Ser Pro Val Gly Thr Lys Asn Ala Ala Gly
225 230 235 240

His Glu Gly Val Arg Asn Lys Asp Ile Asn Gly Val Val Ser Trp Lys
245 250 255

Leu Asn Pro Gln Gln Ile Leu Asp Phe Glu Val Gly Tyr Ser Arg Gln
260 265 270

Gly Asn Ile Tyr Ala Gly Asp Thr Gln Asn Ser Ser Ser Ser Ala Val
275 280 285

Thr Glu Ser Leu Ala Lys Ser Gly Lys Glu Thr Asn Arg Leu Tyr Arg
290 295 300

Gln Asn Tyr Gly Ile Thr His Asn Gly Ile Trp Asp Trp Gly Gln Ser
305 310 315 320

Arg Phe Gly Val Tyr Tyr Glu Lys Thr Asn Asn Thr Arg Met Asn Glu
325 330 335

Gly Leu Ser Gly Gly Gly Glu Gly Arg Ile Leu Ala Gly Glu Lys Phe

340 345 350

Thr Thr Asn Arg Leu Ser Ser Trp Arg Thr Ser Gly Glu Leu Asn Ile
355 360 365

Pro Leu Asn Val Met Val Asp Gln Thr Leu Thr Val Gly Ala Glu Trp
370 375 380

Asn Arg Asp Lys Leu Asp Asp Pro Ser Ser Thr Ser Leu Thr Val Asn
385 390 395 400

Asp Arg Asp Ile Ser Gly Ile Ser Gly Ser Ala Ala Asp Arg Ser Ser
405 410 415

Lys Asn His Ser Gln Ile Ser Ala Leu Tyr Ile Glu Asp Asn Ile Glu
420 425 430

Pro Val Pro Gly Thr Asn Ile Ile Pro Gly Leu Arg Phe Asp Tyr Leu
435 440 445

Ser Asp Ser Gly Gly Asn Phe Ser Pro Ser Leu Asn Leu Ser Gln Glu
450 455 460

Leu Gly Asp Tyr Phe Lys Val Lys Ala Gly Val Ala Arg Thr Phe Lys
465 470 475 480

Ala Pro Asn Leu Tyr Gln Ser Ser Glu Gly Tyr Leu Leu Tyr Ser Lys
485 490 495

Gly Asn Gly Cys Pro Lys Asp Ile Thr Ser Gly Gly Cys Tyr Leu Ile
500 505 510

Gly Asn Lys Asp Leu Asp Pro Glu Ile Ser Val Asn Lys Glu Ile Gly
515 520 525

Leu Glu Phe Thr Trp Glu Asp Tyr His Ala Ser Val Thr Tyr Phe Arg
530 535 540

Asn Asp Tyr Gln Asn Lys Ile Val Ala Gly Asp Asn Val Ile Gly Gln
545 550 555 560

Thr Ala Ser Gly Ala Tyr Ile Leu Lys Trp Gln Asn Gly Gly Lys Ala
565 570 575

Leu Val Asp Gly Ile Glu Ala Ser Met Ser Phe Pro Leu Val Lys Glu
580 585 590

Arg Leu Asn Trp Asn Thr Asn Ala Thr Trp Met Ile Thr Ser Glu Gln
595 600 605

Lys Asp Thr Gly Asn Pro Leu Ser Val Ile Pro Lys Tyr Thr Ile Asn
610 615 620

Asn Ser Leu Asn Trp Thr Ile Thr Gln Ala Phe Ser Ala Ser Phe Asn
625 630 635 640

Trp Thr Leu Tyr Gly Arg Gln Lys Pro Arg Thr His Ala Glu Thr Arg
645 650 655

Ser Glu Asp Thr Gly Gly Leu Ser Gly Lys Glu Leu Gly Ala Tyr Ser
660 665 670

Leu Val Gly Thr Asn Phe Asn Tyr Asp Ile Asn Lys Asn Leu Arg Leu
675 680 685

Asn Val Gly Val Ser Asn Ile Leu Asn Lys Gln Ile Phe Arg Ser Ser
690 695 700

Glu Gly Ala Asn Thr Tyr Asn Glu Pro Gly Arg Ala Tyr Tyr Ala Gly
705 710 715 720

Val Thr Ala Ser Phe
725

<210> 9
<211> 1014
<212> PRT
<213> Escherichia coli
<400> 9

Met Gly Asn Gln Trp Gln Gln Lys Tyr Leu Leu Glu Tyr Asn Glu Leu
1 5 10 15

Val Ser Asn Phe Pro Ser Pro Glu Arg Val Val Ser Asp Tyr Ile Lys
20 25 30

Asn Cys Phe Lys Thr Asp Leu Pro Trp Phe Ser Arg Ile Asp Pro Asp

35 40 45

Asn Ala Tyr Phe Ile Cys Phe Ser Gln Asn Arg Ser Asn Ser Arg Ser
50 55 60

Tyr Thr Gly Trp Asp His Leu Gly Lys Tyr Lys Thr Glu Val Leu Thr
65 70 75 80

Leu Thr Gln Ala Ala Leu Ile Asn Ile Gly Tyr Arg Phe Asp Val Phe
85 90 95

Asp Asp Ala Asn Ser Ser Thr Gly Ile Tyr Lys Thr Lys Ser Ala Asp
100 105 110

Val Phe Asn Glu Glu Asn Glu Glu Lys Met Leu Pro Ser Glu Tyr Leu
115 120 125

His Phe Leu Gln Lys Cys Asp Phe Ala Gly Val Tyr Gly Lys Thr Leu
130 135 140

Ser Asp Tyr Trp Ser Lys Tyr Tyr Asp Lys Phe Lys Leu Leu Leu Lys
145 150 155 160

Asn Tyr Tyr Ile Ser Ser Ala Leu Tyr Leu Tyr Lys Asn Gly Glu Leu
165 170 175

Asp Glu Arg Glu Tyr Asn Phe Ser Met Asn Ala Leu Asn Arg Ser Asp
180 185 190

Asn Ile Ser Leu Leu Phe Phe Asp Ile Tyr Gly Tyr Tyr Ala Ser Asp
195 200 205

Ile Phe Val Ala Lys Asn Asn Asp Lys Val Met Leu Phe Ile Pro Gly
210 215 220

Ala Lys Lys Pro Phe Leu Phe Lys Lys Asn Ile Ala Asp Leu Arg Leu
225 230 235 240

Thr Leu Lys Glu Leu Ile Lys Asp Ser Asp Asn Lys Gln Leu Leu Ser
245 250 255

Gln His Phe Ser Leu Tyr Ser Arg Gln Asp Gly Val Ser Tyr Ala Gly
260 265 270

Val Asn Ser Val Leu His Ala Ile Glu Asn Asp Gly Asn Phe Asn Glu
275 280 285

Ser Tyr Phe Leu Tyr Ser Asn Lys Thr Leu Ser Asn Lys Asp Val Phe
290 295 300

Asp Ala Ile Ala Ile Ser Val Lys Lys Arg Ser Phe Ser Asp Gly Asp
305 310 315 320

Ile Val Ile Lys Ser Asn Ser Glu Ala Gln Arg Asp Tyr Ala Leu Thr
325 330 335

Ile Leu Gln Thr Ile Leu Ser Met Thr Pro Ile Phe Asp Ile Val Val
340 345 350

Pro Glu Val Ser Val Pro Leu Gly Leu Gly Ile Ile Thr Ser Ser Met
355 360 365

Gly Ile Ser Phe Asp Gln Leu Ile Asn Gly Asp Thr Tyr Glu Glu Arg
370 375 380

Arg Ser Ala Ile Pro Gly Leu Ala Thr Asn Ala Val Leu Leu Gly Leu
385 390 395 400

Ser Phe Ala Ile Pro Leu Leu Ile Ser Lys Ala Gly Ile Asn Gln Glu
405 410 415

Val Leu Ser Ser Val Ile Asn Asn Glu Gly Arg Thr Leu Asn Glu Thr
420 425 430

Asn Ile Asp Ile Phe Leu Lys Glu Tyr Gly Ile Ala Glu Asp Ser Ile
435 440 445

Ser Ser Thr Asn Leu Leu Asp Val Lys Leu Lys Ser Ser Gly Gln His
450 455 460

Val Asn Ile Val Lys Leu Ser Asp Glu Asp Asn Gln Ile Val Ala Val
465 470 475 480

Lys Gly Ser Ser Leu Ser Gly Ile Tyr Tyr Glu Val Asp Ile Glu Thr
485 490 495

Gly Tyr Glu Ile Leu Ser Arg Arg Ile Tyr Arg Thr Glu Tyr Asn Asn
500 505 510

Glu Ile Leu Trp Thr Arg Gly Gly Gly Leu Lys Gly Gly Gln Pro Phe
515 520 525

Asp Phe Glu Ser Leu Asn Ile Pro Val Phe Phe Lys Asp Glu Pro Tyr
530 535 540

Ser Ala Val Thr Gly Ser Pro Leu Ser Phe Ile Asn Asp Asp Ser Ser
545 550 555 560

Leu Leu Tyr Pro Asp Thr Asn Pro Lys Leu Pro Gln Pro Thr Ser Glu
565 570 575

Met Asp Ile Val Asn Tyr Val Lys Gly Ser Gly Ser Phe Gly Asp Arg
580 585 590

Phe Val Thr Leu Met Arg Gly Ala Thr Glu Glu Glu Ala Trp Asn Ile
595 600 605

Ala Ser Tyr His Thr Ala Gly Gly Ser Thr Glu Glu Leu His Glu Ile
610 615 620

Leu Leu Gly Gln Gly Pro Gln Ser Ser Leu Gly Phe Thr Glu Tyr Thr
625 630 635 640

Ser Asn Val Asn Ser Ala Asp Ala Ala Ser Arg Arg His Phe Leu Val
645 650 655

Val Ile Lys Val His Val Lys Tyr Ile Thr Asn Asn Asn Val Ser Tyr
660 665 670

Val Asn His Trp Ala Ile Pro Asp Glu Ala Pro Val Glu Val Leu Ala
675 680 685

Val Val Asp Arg Arg Phe Asn Phe Pro Glu Pro Ser Thr Pro Pro Asp
690 695 700

Ile Ser Thr Ile Arg Lys Leu Leu Ser Leu Arg Tyr Phe Lys Glu Ser
705 710 715 720

```
Ile Glu Ser Thr Ser Lys Ser Asn Phe Gln Lys Leu Ser Arg Gly Asn
                725                 730                 735

Ile Asp Val Leu Lys Gly Arg Gly Ser Ile Ser Ser Thr Arg Gln Arg
            740                 745                 750

Ala Ile Tyr Pro Tyr Phe Glu Ala Ala Asn Ala Asp Glu Gln Gln Pro
        755                 760                 765

Leu Phe Phe Tyr Ile Lys Lys Asp Arg Phe Asp Asn His Gly Tyr Asp
    770                 775                 780

Gln Tyr Phe Tyr Asp Asn Thr Val Gly Leu Asn Gly Ile Pro Thr Leu
785                 790                 795                 800

Asn Thr Tyr Thr Gly Glu Ile Pro Ser Asp Ser Ser Ser Leu Gly Ser
                805                 810                 815

Thr Tyr Trp Lys Lys Tyr Asn Leu Thr Asn Glu Thr Ser Ile Ile Arg
            820                 825                 830

Val Ser Asn Ser Ala Arg Gly Ala Asn Gly Ile Lys Ile Ala Leu Glu
        835                 840                 845

Glu Val Gln Glu Gly Lys Pro Val Ile Ile Thr Ser Gly Asn Leu Ser
    850                 855                 860

Gly Cys Thr Thr Ile Val Ala Arg Lys Glu Gly Tyr Ile Tyr Lys Val
865                 870                 875                 880

His Thr Gly Thr Thr Lys Ser Leu Ala Gly Phe Thr Ser Thr Thr Gly
                885                 890                 895

Val Lys Lys Ala Val Glu Val Leu Glu Leu Leu Thr Lys Glu Pro Ile
            900                 905                 910

Pro Arg Val Glu Gly Ile Met Ser Asn Asp Phe Leu Val Asp Tyr Leu
        915                 920                 925

Ser Glu Asn Phe Glu Asp Ser Leu Ile Thr Tyr Ser Ser Ser Glu Lys
    930                 935                 940

Lys Pro Asp Ser Gln Ile Thr Ile Ile Arg Asp Asn Val Ser Val Phe
```

945 950 955 960

Pro Tyr Phe Leu Asp Asn Ile Pro Glu His Gly Phe Gly Thr Ser Ala
965 970 975

Thr Val Leu Val Arg Val Asp Gly Asn Val Val Val Arg Ser Leu Ser
980 985 990

Glu Ser Tyr Ser Leu Asn Ala Asp Ala Ser Glu Ile Ser Val Leu Lys
995 1000 1005

Val Phe Ser Lys Lys Phe
1010

<210> 10
<211> 454
<212> PRT
<213> Escherichia coli
<400> 10

Met Val Asp Met Ile Asn Glu Ser Ala Arg Gln Thr Pro Val Ile Ala
1 5 10 15

Gln Thr Asp Val Leu Val Ile Gly Gly Gly Pro Ala Gly Leu Ser Ala
20 25 30

Ala Ile Ala Ala Gly Arg Leu Gly Ala Arg Thr Met Ile Val Glu Arg
35 40 45

Tyr Gly Ser Leu Gly Gly Val Leu Thr Gln Val Gly Val Glu Ser Phe
50 55 60

Ala Trp Tyr Arg His Pro Gly Thr Glu Asp Cys Glu Gly Ile Cys Arg
65 70 75 80

Glu Tyr Glu Gly Arg Ala Arg Ala Leu Gly Phe Thr Arg Pro Glu Pro
85 90 95

Gln Ser Ile Ser Glu Val Ile Asp Thr Glu Gly Phe Lys Val Val Ala
100 105 110

Asp Gln Met Ile Thr Glu Ser Gly Val Glu Pro Leu Tyr His Ser Trp
115 120 125

Val Val Asp Val Ile Lys Asp Gly Asp Thr Leu Cys Gly Val Ile Val
130 135 140

Glu Asn Lys Ser Gly Arg Gly Ala Ile Leu Ala Lys Arg Ile Val Asp
145 150 155 160

Cys Thr Gly Asp Ala Asp Ile Ala Ala Arg Ala Gly Ala Pro Trp Thr
165 170 175

Lys Arg Ser Lys Asp Gln Leu Met Gly Val Thr Val Met Phe Ser Cys
180 185 190

Ala Gly Val Asp Val Ala Arg Phe Asn Arg Phe Val Ala Glu Glu Leu
195 200 205

Lys Pro Thr Tyr Ala Asp Trp Gly Lys Asn Trp Thr Ile Gln Thr Thr
210 215 220

Gly Lys Glu Asp Pro Met Phe Ser Pro Tyr Met Glu Asp Ile Phe Thr
225 230 235 240

Arg Ala Gln Gln Asp Gly Val Ile Pro Gly Asp Ala Gln Ala Ile Ala
245 250 255

Gly Thr Trp Ser Thr Phe Ser Glu Ser Gly Glu Ala Phe Gln Met Asn
260 265 270

Met Val Tyr Ala Phe Gly Phe Asp Cys Thr Asp Val Phe Asp Leu Thr
275 280 285

Lys Ala Glu Ile Ala Gly Arg Gln Gln Ala Leu Trp Ala Ile Asp Ala
290 295 300

Leu Arg His Tyr Val Pro Gly Phe Glu Asn Val Arg Leu Arg Asn Phe
305 310 315 320

Gly Ala Thr Leu Gly Thr Arg Glu Ser Arg Leu Ile Glu Gly Glu Ile
325 330 335

Arg Ile Ala Asp Asp Tyr Val Leu Asn Gln Gly Arg Cys Ser Asp Ser
340 345 350

Val Gly Ile Phe Pro Glu Phe Ile Asp Gly Ser Gly Tyr Leu Ile Leu

355 360 365

Pro Thr Thr Gly Arg Phe Phe Gln Ile Pro Tyr Gly Cys Leu Val Pro
370 375 380

Gln Lys Val Glu Asn Leu Leu Val Ala Gly Arg Cys Ile Ser Ala Gly
385 390 395 400

Val Val Ala His Thr Ser Met Arg Asn Met Met Cys Cys Ala Val Thr
405 410 415

Gly Glu Ala Ala Gly Thr Ala Ala Val Val Ser Leu Gln Gln Asn Cys
420 425 430

Thr Val Arg Gln Val Ala Ile Pro Asp Leu Gln Asn Thr Leu Gln Gln
435 440 445

Gln Gly Val Arg Leu Ala
450

<210> 11
<211> 253
<212> PRT
<213> Escherichia coli
<400> 11

Met Ser Ala Lys Arg Arg Leu Leu Ile Ala Cys Thr Leu Ile Thr Ala
1 5 10 15

Ile Tyr His Phe Pro Ala Tyr Ser Ser Leu Glu Tyr Lys Gly Thr Phe
20 25 30

Gly Ser Ile Asn Ala Gly Tyr Ala Asp Trp Asn Ser Gly Phe Val Asn
35 40 45

Thr His Arg Gly Glu Val Trp Lys Val Thr Ala Asp Phe Gly Val Asn
50 55 60

Phe Lys Glu Ala Glu Phe Tyr Ser Phe Tyr Glu Ser Asn Val Leu Asn
65 70 75 80

His Ala Val Ala Gly Arg Asn His Thr Val Ser Ala Met Thr His Val
85 90 95

Arg Leu Phe Asp Ser Asp Met Thr Phe Phe Gly Lys Ile Tyr Gly Gln
100 105 110

Trp Asp Asn Ser Trp Gly Asp Asp Leu Asp Met Phe Tyr Gly Phe Gly
115 120 125

Tyr Leu Gly Trp Asn Gly Glu Trp Gly Phe Phe Lys Pro Tyr Ile Gly
130 135 140

Leu His Asn Gln Ser Gly Asp Tyr Val Ser Ala Lys Tyr Gly Gln Thr
145 150 155 160

Asn Gly Trp Asn Gly Tyr Val Val Gly Trp Thr Ala Val Leu Pro Phe
165 170 175

Thr Leu Phe Asp Glu Lys Phe Val Leu Ser Asn Trp Asn Glu Ile Glu
180 185 190

Leu Asp Arg Asn Asp Ala Tyr Thr Glu Gln Gln Phe Gly Arg Asn Gly
195 200 205

Leu Asn Gly Gly Leu Thr Ile Ala Trp Lys Phe Tyr Pro Arg Trp Lys
210 215 220

Ala Ser Val Thr Trp Arg Tyr Phe Asp Asn Lys Leu Gly Tyr Asp Gly
225 230 235 240

Phe Gly Asp Gln Met Ile Tyr Met Leu Gly Tyr Asp Phe
245 250

<210> 12
<211> 492
<212> PRT
<213> Escherichia coli
<400> 12

Met Ala Ser Leu Ile Gly Leu Ala Val Cys Thr Gly Asn Ala Phe Ser
1 5 10 15

Pro Ala Leu Ala Ala Glu Ala Lys Gln Pro Asn Leu Val Ile Ile Met
20 25 30

Ala Asp Asp Leu Gly Tyr Gly Asp Leu Ala Thr Tyr Gly His Gln Ile
35 40 45

Val Lys Thr Pro Asn Ile Asp Arg Leu Ala Gln Glu Gly Val Lys Phe
50 55 60

Thr Asp Tyr Tyr Ala Pro Ala Pro Leu Ser Ser Pro Ser Arg Ala Gly
65 70 75 80

Leu Leu Thr Gly Arg Met Pro Phe Arg Thr Gly Ile Arg Ser Trp Ile
85 90 95

Pro Ser Gly Lys Asp Val Ala Leu Gly Arg Asn Glu Leu Thr Ile Ala
100 105 110

Asn Leu Leu Lys Ala Gln Gly Tyr Asp Thr Ala Met Met Gly Lys Leu
115 120 125

His Leu Asn Ala Gly Gly Asp Arg Thr Asp Gln Pro Gln Ala Gln Asp
130 135 140

Met Gly Phe Asp Tyr Ser Leu Ala Asn Thr Ala Gly Phe Val Thr Asp
145 150 155 160

Ala Thr Leu Asp Asn Ala Lys Glu Arg Pro Arg Tyr Gly Met Val Tyr
165 170 175

Pro Thr Gly Trp Leu Arg Asn Gly Gln Pro Thr Pro Arg Ala Asp Lys
180 185 190

Met Ser Gly Glu Tyr Val Ser Ser Glu Val Val Asn Trp Leu Asp Asn
195 200 205

Lys Lys Asp Ser Lys Pro Phe Phe Leu Tyr Val Ala Phe Thr Glu Val
210 215 220

His Ser Pro Leu Ala Ser Pro Lys Lys Tyr Leu Asp Met Tyr Ser Gln
225 230 235 240

Tyr Met Ser Ala Tyr Gln Lys Gln His Pro Asp Leu Phe Tyr Gly Asp
245 250 255

Trp Ala Asp Lys Pro Trp Arg Gly Val Gly Glu Tyr Tyr Ala Asn Ile
260 265 270

```
Ser Tyr Leu Asp Ala Gln Val Gly Lys Val Leu Asp Lys Ile Lys Ala
        275                 280                 285

Met Gly Glu Glu Asp Asn Thr Ile Val Ile Phe Thr Ser Asp Asn Gly
    290                 295                 300

Pro Val Thr Arg Glu Ala Arg Lys Val Tyr Glu Leu Asn Leu Ala Gly
305                 310                 315                 320

Glu Thr Asp Gly Leu Arg Gly Arg Lys Asp Asn Leu Trp Glu Gly Gly
                325                 330                 335

Ile Arg Val Pro Ala Ile Ile Lys Tyr Gly Lys His Leu Pro Gln Gly
            340                 345                 350

Met Val Ser Asp Thr Pro Val Tyr Gly Leu Asp Trp Met Pro Thr Leu
        355                 360                 365

Ala Lys Met Met Asn Phe Lys Leu Pro Thr Asp Arg Thr Phe Asp Gly
    370                 375                 380

Glu Ser Leu Val Pro Val Leu Glu Gln Lys Ala Leu Lys Arg Glu Lys
385                 390                 395                 400

Pro Leu Ile Phe Gly Ile Asp Met Pro Phe Gln Asp Asp Pro Thr Asp
                405                 410                 415

Glu Trp Ala Ile Arg Asp Gly Asp Trp Lys Met Ile Ile Asp Arg Asn
            420                 425                 430

Asn Lys Pro Lys Tyr Leu Tyr Asn Leu Lys Ser Asp Arg Tyr Glu Thr
        435                 440                 445

Leu Asn Leu Ile Gly Lys Lys Pro Asp Ile Glu Lys Gln Met Tyr Gly
    450                 455                 460

Lys Phe Leu Lys Tyr Lys Thr Asp Ile Asp Asn Asp Ser Leu Met Lys
465                 470                 475                 480

Ala Arg Gly Asp Lys Pro Glu Ala Val Thr Trp Gly
                485                 490
```

<210> 13

<211> 345
<212> PRT
<213> Escherichia coli
<400> 13

Leu Ile Ser Leu Ser Phe Ile Pro Val Met Ser Ala Leu Pro Gly Pro
1 5 10 15

Ile Ala Lys Gly Phe Arg Asn Glu Arg Gly Phe Val Thr Thr Thr Ile
20 25 30

Cys Ala Met Gly Glu Leu Leu Ala Glu Phe Leu Ser Arg Asn Pro His
35 40 45

Gln Lys Phe Thr Gln Pro Gly Glu Phe Ile Gly Pro Phe Pro Ser Gly
50 55 60

Ala Pro Ala Ile Phe Ala Ala Gln Val Ala Lys Leu Ser His Arg Ala
65 70 75 80

Ile Phe Phe Gly Cys Val Gly Asn Asp Asp Phe Ala Arg Leu Ile Ile
85 90 95

Glu Arg Leu Arg His Glu Gly Val Ile Thr Asp Gly Ile His Val Met
100 105 110

Asn Asn Ala Val Thr Gly Thr Ala Phe Val Ser Tyr Gln Asn Pro Gln
115 120 125

Gln Arg Asp Phe Val Phe Asn Ile Pro Asn Ser Ala Cys Gly Leu Phe
130 135 140

Thr Ala Glu His Ile Asp Lys Asp Leu Leu Lys Gln Cys Asn His Leu
145 150 155 160

His Ile Val Gly Ser Ser Leu Phe Ser Phe Arg Met Ile Asp Val Met
165 170 175

Arg Lys Ala Ile Thr Thr Ile Lys Ser Ala Gly Gly Thr Val Ser Phe
180 185 190

Asp Pro Asn Ile Arg Lys Glu Met Leu Ser Ile Pro Glu Met Ala Gln
195 200 205

```
Ala Leu Asp Tyr Leu Ile Glu Tyr Thr Asp Ile Phe Ile Pro Ser Glu
    210                 215                 220

Ser Glu Leu Pro Phe Phe Ala Arg His Lys Asn Leu Ser Glu Glu Gln
225                 230                 235                 240

Ile Val Ser Asp Leu Leu His Gly Gly Val Lys His Val Ala Ile Lys
                245                 250                 255

Arg Ala Gln Arg Gly Ala Ser Tyr Tyr Lys Leu Lys Asn Gly Thr Leu
            260                 265                 270

His Ala Gln His Val Ala Gly His Asp Ile Glu Ile Ile Asp Pro Thr
        275                 280                 285

Gly Ala Gly Asp Cys Phe Gly Ala Thr Phe Ile Thr Leu Phe Leu Ser
    290                 295                 300

Gly Phe Pro Ala His Lys Ala Leu Gln Tyr Ala Asn Ala Ser Gly Ala
305                 310                 315                 320

Leu Ala Val Met Arg Gln Gly Pro Met Glu Gly Ile Ser Ser Leu Ala
                325                 330                 335

Asp Ile Glu Asp Phe Leu Gln Gln His
            340                 345
```

<210> 14
<211> 192
<212> PRT
<213> Escherichia coli
<400> 14

```
Met Tyr Met Pro Gly Lys Gln Met Leu Cys Cys Ile Leu Ile Ser Ile
1               5                   10                  15

Ile Ser Glu Gly Asp Met Lys Ile Phe Ile Ser Leu Phe Leu Phe Ile
            20                  25                  30

Ile Ser Thr Asn Ser Phe Ala Asp Asp Ile Thr His Ala Gly Val Val
        35                  40                  45

Arg Ile Glu Gly Leu Ile Thr Glu Lys Thr Cys Ile Ile Ser Asp Glu
    50                  55                  60
```

Ser Lys Asn Phe Thr Val Asn Met Pro Asp Val Pro Ser Ser Ser Val
65 70 75 80

Arg Ser Ala Gly Asp Val Thr Glu Lys Val Tyr Phe Ser Ile Thr Leu
85 90 95

Thr Arg Cys Gly Ser Asp Val Gly Asn Ala Tyr Ile Lys Phe Thr Gly
100 105 110

Asn Thr Val Ser Glu Asp Ala Ser Leu Tyr Lys Leu Glu Asp Gly Ser
115 120 125

Val Glu Gly Leu Ala Leu Thr Ile Phe Asp Lys Asn Lys Gly Ser Ile
130 135 140

Ser Asn Asp Val Lys Ser Met Val Phe Ser Leu Thr Ser Ser Val Asp
145 150 155 160

Asn Ile Leu His Phe Phe Ala Ala Tyr Lys Ala Leu Lys Asn Asn Val
165 170 175

Gln Pro Gly Asp Ala Asn Ala Ser Val Ser Phe Ile Val Thr Tyr Asp
180 185 190

<210> 15
<211> 201
<212> PRT
<213> Escherichia coli
<400> 15

Met Ile Lys Phe Arg Leu Tyr Ile Pro Pro Val Ile Leu Gly Phe Val
1 5 10 15

Ile Val Pro Leu Leu Val Trp Pro Thr Val Ile Ala Leu Ala Val Leu
20 25 30

Ile Phe Thr Leu Thr Phe Leu Ala Glu Ile Ile Phe Ser Phe Pro Leu
35 40 45

Leu Val Val Arg Ile Ser Leu Gln Glu Leu Gln Leu Glu Leu Leu Val
50 55 60

Val Tyr Ala Leu Phe Phe Ser Val Met Gly Gly Ile Gly Trp Gln Phe
65 70 75 80

```
Ser Arg Arg Thr Pro Pro Glu Leu Lys Asn Arg Leu His Cys Trp Leu
                85                  90                  95

Val Phe Ser Pro Val Tyr Phe Trp Leu Ile Leu Ser Asn Phe Ile Leu
            100                 105                 110

Tyr Ile Ser Pro Glu Lys Ser Ala Leu Leu Glu Asn Ile Arg Asn Phe
        115                 120                 125

Phe Leu Thr Phe Val Trp Leu Pro Leu Asn Phe Ser Pro Phe Trp Pro
    130                 135                 140

Gln Pro Trp Thr Asp Phe Val Gly Pro Ile Ser Ala Gln Leu Gly Phe
145                 150                 155                 160

Ala Leu Gly Tyr Tyr Cys Gln Trp Arg Ser Lys Asn Arg Ser His Arg
                165                 170                 175

Lys Lys Trp Gly Asp Trp Val Thr Cys Leu Ser Leu Ala Ile Leu Ala
            180                 185                 190

Leu Gly Pro Leu Phe Asn Tyr Leu Gln
        195                 200
```

<210> 16
<211> 234
<212> PRT
<213> Escherichia coli
<400> 16

```
Met Lys Phe Asn Leu Ser Asn Leu Ser Ala Val Leu Leu Ala Ser Gly
1               5                   10                  15

Met Leu Met Ser Thr Ala Val Thr Ala Ala Pro Gly Asp Ala Thr Gln
            20                  25                  30

Phe Gly Gly Ala Asp Thr Asp Trp Ser Thr Val Asp Tyr Pro Arg Leu
        35                  40                  45

Thr Asp Met Asp Asp Asn Val Asp Ser Met Gly Gly Lys Ile Arg Phe
    50                  55                  60

Thr Gly Arg Val Val Lys Ala Thr Cys Lys Val Ala Thr Asp Ser Lys
```

65 70 75 80

Gln Ile Glu Val Val Leu Pro Val Val Pro Ser Asn Leu Phe Thr Gly
85 90 95

Ile Asp Val Glu Ala Gln Gly Ala Ser Asn Gln Thr Asp Phe Asn Ile
100 105 110

Asn Leu Thr Glu Cys Ser Asn Thr Asp Asp Gln Lys Ile Glu Phe Arg
115 120 125

Phe Thr Gly Thr Ala Asp Ser Ala Asn Lys Thr Leu Ala Asn Glu Val
130 135 140

Glu Gly Ser Thr Asp Ala Asp Asn Ser Gly Asn Ala Gly Ala Thr Gly
145 150 155 160

Val Gly Ile Arg Ile Tyr Ser Lys Gly Thr Thr Asn Asn Gly Leu Ile
165 170 175

Asn Leu Asn Thr Thr Ala Ala Glu Gly Ser Ala Ser Thr Ala Ala Tyr
180 185 190

Thr Ile Pro Gly Asn Ala Thr Thr His Asp Phe Ser Ala Ala Phe Thr
195 200 205

Ala Gly Tyr Ala Gln Asn Gly Ser Thr Val Ala Pro Gly Val Val Lys
210 215 220

Ser Thr Ala Ser Phe Val Val Leu Tyr Glu
225 230

<210> 17
<211> 336
<212> PRT
<213> Escherichia coli
<400> 17

Met Arg Ile His Thr Tyr Trp Tyr Arg Arg Tyr Phe Ile Leu Leu Ile
1 5 10 15

Ile Ile Phe Ser Asn Val Leu Ser Ser Ile Ala Asn Ala Glu Asp Met
20 25 30

Gly Arg Glu Arg Ala Tyr Cys Tyr Pro Gly Ser Pro Ser Asn Asn Thr
35 40 45

Thr Pro Ala Ser Phe Ser Tyr Asn Phe Gly Thr Ile Val Val Ser Asp
50 55 60

Val Asn Lys Asn Ala Pro Gly Thr Val Leu Pro Ser Gln Ile Trp Lys
65 70 75 80

Val Gly Thr Tyr Lys Ala Tyr Cys Asn Ser Leu Asp Asp Tyr Glu Ile
85 90 95

Tyr Phe Ser Ala Val Ser Gly Ile Asp Pro Ser Gly Ala Ser Gly Asp
100 105 110

His Gln Gly Ser Asp Val Phe Ile Pro Leu Thr His Glu Ile Ser Val
115 120 125

Ser Thr His Ile Lys Leu Tyr Asn Gln Asn Gly Thr Met Thr Asp Lys
130 135 140

Ile Val Pro Phe Glu Asn Tyr Asn Thr Asn Tyr Pro Gly Asp Arg Ser
145 150 155 160

Lys Pro Ser Asn Trp Ala Ser Gly Thr Glu Gly Tyr Ile Lys Ile Arg
165 170 175

Ile Asp Lys Lys Ile Ile Ser Asp Val Ser Leu Ser Asn Val Leu Leu
180 185 190

Val Ser Leu Tyr Val Ser Gln Ile Pro Thr Glu His Gly Pro Ile Pro
195 200 205

Val Phe Asn Ala Tyr Ile Gly Asn Leu Asn Ile Gln Val Pro Gln Gly
210 215 220

Cys Thr Ile Asn Glu Gly Thr Ser Phe Thr Val Asn Met Pro Asp Val
225 230 235 240

Trp Ala Ser Glu Leu Ser Arg Ala Gly Ala Gly Ala Lys Pro Ala Gly
245 250 255

Val Thr Pro Val Ala Thr Thr Ile Pro Ile Asn Cys Thr Asn Lys Asp

260 265 270

Thr Asp Ala Val Met Thr Leu Val Phe Asp Gly Asn Ile Ser Ala Thr
275 280 285

Arg Asp Thr Asn Gly Lys Gln Ser Ile Ile Gln Ala Gln Asp Asn Pro
290 295 300

Asp Val Gly Ile Met Ile Met Asp Ser Gln Gln Asn Ser Val Asp Leu
305 310 315 320

Asn Ala Leu Ala Thr Ser Val Gly Val Pro Phe Arg Leu Val Glu Asn
325 330 335

<210> 18
<211> 864
<212> PRT
<213> Escherichia coli
<400> 18

Met Asn Leu Lys Leu Lys Arg Cys Glu Tyr Trp Met Ala Ala Gln Lys
1 5 10 15

Gln Met Lys Arg Val Val Pro Leu Leu Leu Val Ile Met Pro Ala Cys
20 25 30

Ser Ile Ala Gly Met Arg Phe Asn Pro Ala Phe Leu Ser Gly Asp Thr
35 40 45

Glu Ala Val Ala Asp Leu Ser Arg Phe Glu Lys Gly Met Thr Tyr Leu
50 55 60

Pro Gly Ser Tyr Glu Val Glu Val Trp Val Asn Asp Ser Pro Leu Leu
65 70 75 80

Ser Arg Thr Val Thr Phe Lys Ala Asp Asp Glu Asn Gln Leu Ile Pro
85 90 95

Cys Leu Ser Leu Ala Asp Leu Leu Ser Leu Gly Ile Asn Lys Asn Ala
100 105 110

Leu Pro Glu Gln Ala Leu Ala Ser Ser Glu Asn Ser Cys Leu Asp Leu
115 120 125

```
Arg Ile Trp Phe Pro Asp Val His Tyr Met Pro Glu Leu Asp Ala Gln
    130                 135                 140

Arg Leu Lys Leu Thr Phe Pro Gln Ala Ile Ile Lys Arg Asp Ala Arg
145                 150                 155                 160

Gly Tyr Ile Pro Pro Glu Gln Trp Asp Asn Gly Ile Thr Ala Phe Leu
                165                 170                 175

Leu Asn Tyr Asp Phe Ser Gly Asn Asn Asp Arg Gly Asp Tyr Ser Ser
            180                 185                 190

Asn Asn Tyr Tyr Leu Asn Leu Arg Ala Gly Ile Asn Ile Gly Ala Trp
        195                 200                 205

Arg Phe Arg Asp Tyr Ser Thr Trp Ser Arg Gly Ser Asn Ser Ala Gly
    210                 215                 220

Lys Leu Glu His Ile Ser Ser Thr Leu Gln Arg Val Ile Ile Pro Phe
225                 230                 235                 240

Arg Ser Glu Leu Thr Leu Gly Asp Thr Trp Ser Ser Ser Asp Val Phe
                245                 250                 255

Asp Ser Val Ser Ile Arg Gly Ile Lys Leu Glu Ser Asp Glu Asn Met
            260                 265                 270

Leu Pro Asp Ser Gln Ser Gly Phe Ala Pro Thr Val Arg Gly Ile Ala
        275                 280                 285

Lys Ser Arg Ala Gln Val Thr Ile Lys Gln Asn Gly Tyr Val Ile Tyr
    290                 295                 300

Gln Thr Tyr Met Pro Pro Gly Pro Phe Glu Ile Ser Asp Leu Asn Pro
305                 310                 315                 320

Thr Ser Ser Ala Gly Asp Leu Glu Val Thr Ile Lys Glu Ser Asp Asn
                325                 330                 335

Ser Glu Thr Val Tyr Thr Val Pro Tyr Ala Ala Val Pro Ile Leu Gln
            340                 345                 350

Arg Glu Gly His Leu Lys Tyr Ser Thr Thr Val Gly Gln Tyr Arg Ser
```

```
        355                 360                 365

Asn Ser Tyr Asn Gln Lys Ser Pro Tyr Val Phe Gln Gly Glu Leu Ile
    370                 375                 380

Trp Gly Leu Pro Trp Asp Ile Thr Ala Tyr Gly Gly Ala Gln Phe Ser
385                 390                 395                 400

Glu Asp Tyr Arg Ala Leu Ala Leu Gly Leu Gly Leu Asn Leu Gly Val
                405                 410                 415

Phe Gly Ala Thr Ser Phe Asp Val Thr Gln Ala Asn Ser Ser Leu Val
            420                 425                 430

Asp Gly Ser Lys His Gln Gly Gln Ser Tyr Arg Phe Leu Tyr Ser Lys
        435                 440                 445

Ser Leu Val Gln Thr Gly Thr Ala Phe His Ile Ile Gly Tyr Arg Tyr
    450                 455                 460

Ser Thr Gln Gly Phe Tyr Thr Leu Ser Asp Thr Thr Tyr Gln Gln Met
465                 470                 475                 480

Ser Gly Thr Val Val Asp Pro Lys Thr Leu Asp Asp Lys Asp Tyr Val
                485                 490                 495

Tyr Asn Trp Asn Asp Phe Tyr Asn Leu Arg Tyr Ser Lys Arg Gly Lys
            500                 505                 510

Phe Gln Ala Ser Val Ser Gln Pro Phe Gly Asn Tyr Gly Ser Met Tyr
        515                 520                 525

Leu Ser Ala Ser Gln Gln Thr Tyr Trp Asn Thr Asp Lys Lys Asp Ser
    530                 535                 540

Leu Tyr Gln Val Gly Tyr Asn Thr Ser Ile Lys Gly Ile Tyr Leu Asn
545                 550                 555                 560

Val Ala Trp Asn Tyr Ser Lys Ser Pro Gly Thr Asn Ala Asp Lys Ile
                565                 570                 575

Val Ser Leu Asn Val Ser Leu Pro Ile Ser Asn Trp Leu Ser Ser Thr
            580                 585                 590
```

Asn Asp Gly Arg Ser Ser Ser Asn Ala Met Thr Ala Thr Tyr Gly Tyr
595 600 605

Ser Gln Asp Asn His Gly Gln Val Asn Gln Tyr Thr Gly Val Ser Gly
610 615 620

Ser Leu Leu Glu Gln His Asn Leu Ser Tyr Asn Ile Gln His Gly Phe
625 630 635 640

Ala Asn Gln Asp Asn Ser Ser Ser Gly Ser Val Gly Val Asn Tyr Arg
645 650 655

Gly Ala Tyr Gly Ser Leu Asn Ser Ala Tyr Ser Tyr Asp Asn Glu Gly
660 665 670

Asn Gln Gln Ile Asn Tyr Gly Ile Ser Gly Ala Leu Val Val His Glu
675 680 685

Asn Gly Leu Thr Leu Ser Gln Pro Leu Gly Glu Thr Asn Val Leu Ile
690 695 700

Lys Ala Pro Gly Ala Asn Asn Val Asp Val Gln Arg Gly Thr Gly Ile
705 710 715 720

Ser Thr Asp Trp Arg Gly Tyr Ala Val Val Pro Tyr Ala Thr Glu Tyr
725 730 735

Arg Arg Asn Asn Ile Ser Leu Asp Pro Met Ser Met Asn Met His Thr
740 745 750

Glu Leu Asp Ile Thr Ser Thr Glu Val Ile Pro Gly Lys Gly Ala Leu
755 760 765

Val Arg Ala Glu Phe Ala Ala His Ile Gly Ile Arg Gly Leu Phe Thr
770 775 780

Val Arg Tyr Arg Asn Lys Ser Val Pro Phe Gly Ala Thr Ala Ser Ala
785 790 795 800

Gln Ile Lys Asn Ser Ser Gln Ile Thr Gly Ile Val Gly Asp Asn Gly
805 810 815

Gln Leu Tyr Leu Ser Gly Leu Pro Leu Glu Gly Val Ile Asn Ile Gln
820 825 830

Trp Gly Asp Gly Val Gln Gln Lys Cys Gln Ala Asn Tyr Lys Leu Pro
835 840 845

Glu Thr Glu Leu Asp Asn Pro Val Ser Tyr Ala Thr Leu Glu Cys Arg
850 855 860

<210> 19
<211> 169
<212> PRT
<213> Escherichia coli
<400> 19

Met Gly Ala Ile Tyr Val Lys Arg Leu Ile Leu Ser Val Ala Leu Ile
1 5 10 15

Ile Pro Ile Ala Ser Asn Ala Ser Asp Ala Leu Asn Gln Pro Ser Ser
20 25 30

Ser Leu Asn Asp Gly Val Glu Thr Phe Phe Ile Ser Cys Phe Asp Met
35 40 45

Pro Gln Glu Thr Thr Thr Asp Met Asp Ala Cys Gln Arg Val Gln Leu
50 55 60

Ala Gln Val Ser Trp Val Lys Asn Lys Tyr Ser Val Ala Ala Leu Asn
65 70 75 80

Arg Leu Lys Gln Asp Asn Lys Asp Asp Pro Gln Arg Leu Gln Glu Leu
85 90 95

Thr Ala Ser Phe Asn Ala Glu Ser Glu Ala Trp Thr Glu Leu Ile Glu
100 105 110

Lys Ala Ser Lys Ser Val Gln Val Asp Tyr Val Gly Gly Thr Ile Ala
115 120 125

Gly Thr Ala Val Ala Ser Arg Gln Ile Gly Leu Leu Glu Leu Gln Ser
130 135 140

His Asp Ile Trp Glu His Trp Leu Arg Ser Arg Gly Leu Asn Ser Ser
145 150 155 160

Ser Phe Ala Arg Thr Lys Val Gln Ile
165

<210> 20
<211> 713
<212> PRT
<213> Escherichia coli
<400> 20

Met Ala Met Phe Thr Pro Ser Phe Ser Gly Leu Lys Gly Arg Ala Leu
1 5 10 15

Phe Ser Leu Leu Phe Ala Ala Pro Met Ile His Ala Thr Asp Ser Val
20 25 30

Thr Thr Lys Asp Gly Glu Thr Ile Thr Val Thr Ala Asp Ala Asn Thr
35 40 45

Ala Thr Glu Ala Thr Asp Gly Tyr Gln Pro Leu Ser Thr Ser Thr Ala
50 55 60

Thr Leu Thr Asp Met Pro Met Leu Asp Ile Pro Gln Val Val Asn Thr
65 70 75 80

Val Ser Asp Gln Val Leu Glu Asn Gln Asn Ala Thr Thr Leu Asp Glu
85 90 95

Ala Leu Tyr Asn Val Ser Asn Val Val Gln Thr Asn Thr Leu Gly Gly
100 105 110

Thr Gln Asp Ala Phe Val Arg Arg Gly Phe Gly Ala Asn Arg Asp Gly
115 120 125

Ser Ile Met Thr Asn Gly Leu Arg Thr Val Leu Pro Arg Ser Phe Asn
130 135 140

Ala Ala Thr Glu Arg Val Glu Val Leu Lys Gly Pro Ala Ser Thr Leu
145 150 155 160

Tyr Gly Ile Leu Asp Pro Gly Gly Leu Ile Asn Val Val Thr Lys Arg
165 170 175

Pro Glu Lys Thr Phe His Gly Ser Val Ser Ala Thr Ser Ser Ser Phe

180 185 190

Gly Gly Gly Thr Gly Gln Leu Asp Ile Thr Gly Pro Ile Glu Gly Thr
195 200 205

Gln Leu Ala Tyr Arg Leu Thr Gly Glu Val Gln Asp Glu Asp Tyr Trp
210 215 220

Arg Asn Phe Gly Lys Glu Arg Ser Thr Phe Ile Ala Pro Ser Leu Thr
225 230 235 240

Trp Phe Gly Asp Asn Ala Thr Val Thr Met Leu Tyr Ser His Arg Asp
245 250 255

Tyr Lys Thr Pro Phe Asp Arg Gly Thr Ile Phe Asp Leu Thr Thr Lys
260 265 270

Gln Pro Val Asn Val Asp Arg Lys Ile Arg Phe Asp Glu Pro Phe Asn
275 280 285

Ile Thr Asp Gly Gln Ser Asp Leu Ala Gln Leu Asn Ala Glu Tyr His
290 295 300

Leu Asn Ser Gln Trp Thr Ala Arg Phe Asp Tyr Ser Tyr Ser Gln Asp
305 310 315 320

Lys Tyr Ser Asp Asn Gln Ala Arg Val Thr Ala Tyr Asp Ala Thr Thr
325 330 335

Gly Thr Leu Thr Arg Arg Val Asp Ala Thr Gln Gly Ser Thr Gln Arg
340 345 350

Met His Ala Thr Arg Ala Asp Leu Gln Gly Asn Val Asp Ile Ala Gly
355 360 365

Phe Tyr Asn Glu Ile Leu Gly Gly Val Ser Tyr Glu Tyr Tyr Asp Leu
370 375 380

Leu Arg Thr Asp Met Ile Arg Cys Lys Lys Ala Lys Asp Phe Asn Ile
385 390 395 400

Tyr Asn Pro Val Tyr Gly Asn Thr Ser Lys Cys Thr Thr Val Ser Ala
405 410 415

```
Ser Asp Ser Asp Gln Thr Ile Lys Gln Glu Asn Tyr Ser Ala Tyr Ala
            420                 425                 430

Gln Asp Ala Leu Tyr Leu Thr Asp Asn Trp Ile Ala Val Ala Gly Ile
        435                 440                 445

Arg Tyr Gln Tyr Tyr Thr Gln Tyr Ala Gly Lys Gly Arg Pro Phe Asn
    450                 455                 460

Val Asn Thr Asp Ser Arg Asp Glu Gln Trp Thr Pro Lys Leu Gly Leu
465                 470                 475                 480

Val Tyr Lys Leu Thr Pro Ser Val Ser Leu Phe Ala Asn Tyr Ser Gln
                485                 490                 495

Thr Phe Met Pro Gln Ser Ser Ile Ala Ser Tyr Ile Gly Asp Leu Pro
            500                 505                 510

Pro Glu Ser Ser Asn Ala Tyr Glu Val Gly Ala Lys Phe Glu Leu Phe
        515                 520                 525

Asp Gly Ile Thr Ala Asp Ile Ala Leu Phe Asp Ile His Lys Arg Asn
    530                 535                 540

Val Leu Tyr Thr Glu Ser Ile Gly Asp Glu Thr Ile Ala Lys Thr Ala
545                 550                 555                 560

Gly Arg Val Arg Ser Arg Gly Val Glu Val Asp Leu Ala Gly Ala Leu
                565                 570                 575

Thr Glu Asn Ile Asn Ile Ile Ala Ser Tyr Gly Tyr Thr Asp Ala Lys
            580                 585                 590

Val Leu Glu Asp Pro Asp Tyr Ala Gly Lys Pro Leu Pro Asn Val Pro
        595                 600                 605

Arg His Thr Gly Ser Leu Phe Leu Thr Tyr Asp Ile His Asn Met Pro
    610                 615                 620

Gly Asn Asn Thr Leu Thr Phe Gly Gly Gly Gly His Gly Val Ser Arg
625                 630                 635                 640
```

```
Arg Ser Ala Thr Asn Gly Ala Asp Tyr Tyr Leu Pro Gly Tyr Phe Val
                645                 650                 655

Ala Asp Ala Phe Ala Ala Tyr Lys Met Lys Leu Gln Tyr Pro Val Thr
            660                 665                 670

Leu Gln Leu Asn Val Lys Asn Leu Phe Asp Lys Thr Tyr Tyr Thr Ser
        675                 680                 685

Ser Ile Ala Thr Asn Asn Leu Gly Asn Gln Ile Gly Asp Pro Arg Glu
    690                 695                 700

Val Gln Phe Thr Val Lys Met Glu Phe
705                 710
```

<210> 21
<211> 606
<212> PRT
<213> Escherichia coli
<400> 21

```
Met Lys Ile Ser Trp Asn Tyr Ile Phe Lys Asn Lys Trp Arg Phe His
1               5                   10                  15

Ile Thr Ser Ile Ser Leu Phe Leu Ile Met Leu Ala Val Ser Ile Ala
            20                  25                  30

Phe Leu His Leu Arg Phe Asn Thr Leu Ser Ser Thr Asp Lys Met Arg
        35                  40                  45

Leu Glu Met Tyr Lys Ser Thr Leu Tyr Ser Thr Ile Glu Gln Phe Tyr
    50                  55                  60

Val Leu Pro Tyr Met Leu Ser Thr Asp His Ile Ile Arg Gln Ala Val
65                  70                  75                  80

Ile Thr Pro Asp Asp Met Thr Ser Ser Glu Leu Asn Gln Arg Ile Ala
                85                  90                  95

His Phe Asn Thr Gln Leu Lys Thr Ala Ala Ile Phe Ile Leu Asp Thr
            100                 105                 110

Gln Gly Lys Ala Ile Ala Ser Ser Asn Trp Gln Asp Pro Gly Ser Tyr
        115                 120                 125
```

```
Val Gly Gln Asn Tyr Ser Tyr Arg Pro Tyr Tyr Lys His Ala Met Ser
    130                 135                 140

Gly Leu Asn Gly Arg Phe Tyr Gly Ile Gly Ser Thr Thr Asn Thr Pro
145                 150                 155                 160

Gly Phe Phe Leu Ser Thr Ser Ile Lys Asp Lys Gly Lys Ile Val Gly
                165                 170                 175

Val Val Val Val Lys Ile Ser Leu Asn Glu Ile Glu Lys Ala Trp Ala
            180                 185                 190

Glu Gly Pro Glu Asn Ile Ile Val Asn Asp Glu His Gly Ile Ile Phe
        195                 200                 205

Leu Ser Ser Lys Ser Pro Trp Arg Met Arg Thr Leu Gln Pro Leu Pro
    210                 215                 220

Val Gln Ala Lys Gln Lys Leu Gln Ser Thr Arg Gln Tyr Ser Leu Asp
225                 230                 235                 240

Asn Leu Leu Pro Ala Asp Tyr Tyr Pro Cys Tyr Thr Val Ser Asn Phe
                245                 250                 255

Thr Phe Leu Lys Asp Lys Lys Glu Gln Leu Cys Leu Phe Pro Gln Tyr
            260                 265                 270

Tyr Thr Gln Gln Ile Ala Ile Pro Glu Phe Asn Trp Lys Met Thr Ile
        275                 280                 285

Met Val Pro Leu Asp Asn Leu Tyr Trp Ser Trp Ala Ile Ser Leu Val
    290                 295                 300

Ile Thr Leu Ile Ile Tyr Leu Leu Phe Leu Leu Phe Ile Lys Tyr Trp
305                 310                 315                 320

Arg Met Arg Ser His Ala Gln Gln Leu Leu Thr Leu Ala Asn Glu Thr
                325                 330                 335

Leu Glu Lys Gln Val Lys Glu Arg Thr Ser Ala Leu Glu Leu Ile Asn
            340                 345                 350
```

Gln Lys Leu Ile Gln Glu Ile Lys Glu Arg Ser Gln Ala Glu Gln Val
355 360 365

Leu Gln Ile Thr Arg Ser Glu Leu Ala Glu Ser Ser Lys Leu Ala Ala
370 375 380

Leu Gly Gln Met Ala Thr Glu Ile Ala His Glu Gln Asn Gln Pro Leu
385 390 395 400

Ala Ala Ile His Ala Leu Thr Asp Asn Ala Arg Thr Met Leu Lys Lys
405 410 415

Glu Met Tyr Pro Gln Val Glu Gln Asn Leu Lys His Ile Ile Ser Val
420 425 430

Ile Glu Arg Met Thr Gln Leu Ile Ser Glu Leu Lys Ala Phe Ala Ser
435 440 445

Arg His Arg Val Pro Lys Gly Ser Ala Asp Val Ile Lys Val Met Tyr
450 455 460

Ser Ala Val Ala Leu Leu Asn His Ser Met Glu Lys Asn Asn Ile Glu
465 470 475 480

Arg Arg Ile Lys Ala Pro Ser Met Pro Leu Phe Val Asn Cys Asp Glu
485 490 495

Leu Gly Leu Glu Gln Ile Phe Ser Asn Leu Ile Ser Asn Ala Leu Asp
500 505 510

Ser Met Glu Gly Ser Ser Tyr Lys Arg Leu Asp Ile Ala Ile Arg Gln
515 520 525

Ala Asn Asn Lys Val Ile Ile Thr Ile Lys Asp Ser Gly Gly Gly Phe
530 535 540

Ala Pro Glu Val Val Asp Arg Ile Phe Glu Pro Phe Phe Thr Thr Lys
545 550 555 560

Arg Arg Gly Met Gly Leu Gly Leu Ala Ile Val Ser Glu Ile Val Arg
565 570 575

Asn Ser Asn Gly Ala Leu His Ala Ser Asn His Pro Glu Gly Gly Ala
580 585 590

Val Met Thr Leu Thr Trp Pro Glu Trp Gly Glu Glu His Glu
595 600 605

<210> 22
<211> 101
<212> PRT
<213> Escherichia coli
<400> 22

Val Leu Thr Pro Gln His Leu Arg Cys Val Leu Thr Cys Ser Asp Leu
1 5 10 15

Leu Thr Leu Leu Ser Gly Thr Val Met Ser Gln Met Pro Leu Tyr Phe
20 25 30

Leu Asn Thr Gln Lys Lys Leu Thr Ala His Tyr Glu Trp Leu Gln Ile
35 40 45

Asn Leu Thr Asp Thr Tyr Glu Leu Val Lys Arg Leu Met Pro Ile Pro
50 55 60

Ser Leu Asp Val Val Val Lys Val Gly Lys Leu Val Leu Pro Glu Lys
65 70 75 80

Gly His His Gly Phe Tyr Pro Glu Ala Gly Val Val Tyr Arg Thr Val
85 90 95

Ala Pro Glu Asn Pro
100

<210> 23
<211> 263
<212> PRT
<213> Escherichia coli
<400> 23

Met Met Lys Asn Thr Gly Tyr Ile Leu Ala Leu Cys Leu Thr Ala Ser
1 5 10 15

Gly His Val Leu Ala His Asp Val Trp Ile Thr Gly Lys Gln Ala Glu
20 25 30

Asn Asn Val Thr Ala Glu Ile Gly Tyr Gly His Asn Phe Pro Ser Lys

35 40 45

Gly Thr Ile Pro Asp Arg Arg Asp Phe Phe Glu Asn Pro Arg Leu Tyr
50 55 60

Asn Gly Lys Glu Thr Ile Thr Leu Lys Pro Ala Ser Thr Asp Tyr Val
65 70 75 80

Tyr Lys Thr Glu Ser Ala Ser Lys Asp Asn Gly Tyr Val Leu Ser Thr
85 90 95

Tyr Met Lys Pro Gly Tyr Trp Ser Arg Thr Ser Ser Gly Trp Lys Pro
100 105 110

Val Ser Arg Glu Gly Arg Asn Asp Val Ala Tyr Cys Glu Phe Val Thr
115 120 125

Lys Tyr Ala Lys Ser Phe Ile Pro Gly Glu Gln Gln Met Pro Ala Gln
130 135 140

Leu Tyr Gln Ser Pro Thr Gly His Glu Leu Glu Ile Ile Pro Leu Ser
145 150 155 160

Asp Ile Ser Arg Phe Ser Glu Asn Val Lys Leu Lys Val Leu Tyr Lys
165 170 175

Thr Ser Pro Leu Ala Gly Ala Ile Met Glu Leu Asp Ser Val Ser Tyr
180 185 190

Leu Thr Ser Ser Arg His Thr His Ala Val Glu His Lys His Pro Val
195 200 205

His Lys Ala Glu Leu Thr Phe Val Thr Asn Glu Asp Gly Ile Val Thr
210 215 220

Val Pro Ser Leu His Ile Gly Gln Trp Leu Ala Lys Val Gln Asn Lys
225 230 235 240

Lys Ser Phe Gln Asp Lys Ser Leu Cys Asp Glu Thr Val Asp Val Ala
245 250 255

Thr Leu Ser Phe Ser Arg Asn
260

<210> 24
<211> 378
<212> PRT
<213> Escherichia coli
<400> 24

Met Gly Lys Ile Lys Tyr Trp Leu Ile Val Gly Phe Ile Ile Leu Phe
1 5 10 15

Ala Ile Phe Tyr Ile Ala Ile Ser Asp Arg Asp Ser Thr Leu Ser Arg
20 25 30

Leu Lys Ser Ala Gly Glu Asn Gly Asp Val Glu Ala Gln Tyr Ala Leu
35 40 45

Gly Leu Met Tyr Leu Tyr Gly Glu Ile Leu Asp Val Asp Tyr Gln Gln
50 55 60

Ala Lys Ile Trp Tyr Glu Lys Ala Ala Asp Gln Asn Asp Pro Arg Ala
65 70 75 80

Gln Ala Lys Leu Gly Val Met Tyr Ala Asn Gly Leu Gly Val Asn Gln
85 90 95

Asp Tyr Gln Gln Ser Lys Leu Trp Tyr Glu Lys Ala Ala Ala Gln Asn
100 105 110

Asp Val Asp Ala Gln Phe Leu Leu Gly Glu Met Tyr Asp Asp Gly Leu
115 120 125

Gly Val Ser Gln Asp Tyr Gln His Ala Lys Met Trp Tyr Glu Lys Ala
130 135 140

Ala Ala Gln Asn Asp Glu Arg Ala Gln Val Asn Leu Ala Val Leu Tyr
145 150 155 160

Ala Lys Gly Asn Gly Val Glu Gln Asp Tyr Arg Gln Ala Lys Ser Trp
165 170 175

Tyr Glu Lys Ala Ala Ala Gln Asn Ser Pro Asp Ala Gln Phe Ala Leu
180 185 190

Gly Ile Leu Tyr Ala Asn Ala Asn Gly Val Glu Gln Asp Tyr Gln Gln

195 200 205

Ala Lys Asp Trp Tyr Glu Lys Ala Ala Glu Gln Asn Phe Ala Asn Ala
210 215 220

Gln Phe Asn Leu Gly Met Leu Tyr Tyr Lys Gly Glu Gly Val Lys Gln
225 230 235 240

Asn Phe Arg Gln Ala Arg Glu Trp Phe Glu Lys Ala Ala Ser Gln Asn
245 250 255

Gln Pro Asn Ala Gln Tyr Asn Leu Gly Gln Ile Tyr Tyr Tyr Gly Gln
260 265 270

Gly Val Thr Gln Ser Tyr Arg Gln Ala Lys Asp Trp Phe Glu Lys Ala
275 280 285

Ala Glu Lys Gly His Val Asp Ala Gln Tyr Asn Leu Gly Val Ile Tyr
290 295 300

Glu Asn Gly Glu Gly Val Ser Gln Asn Tyr Gln Gln Ala Lys Ala Trp
305 310 315 320

Tyr Glu Lys Ala Ala Ser Gln Asn Asp Ala Gln Ala Gln Phe Glu Leu
325 330 335

Gly Val Met Asn Glu Leu Gly Gln Gly Glu Ser Ile Asp Leu Lys Gln
340 345 350

Ala Arg His Tyr Tyr Glu Arg Ser Cys Asn Asn Gly Leu Lys Lys Gly
355 360 365

Cys Glu Arg Leu Lys Glu Leu Leu Tyr Lys
370 375

<210> 25
<211> 654
<212> PRT
<213> Escherichia coli
<400> 25

Met Asn Val Ile Arg Thr Val Ile Cys Thr Leu Ile Ile Leu Pro Val
1 5 10 15

```
Gly Leu Gln Ala Ala Thr Ser His Ser Ser Met Val Lys Asp Thr Ile
            20                  25                  30

Thr Ile Val Ala Thr Gly Asn Gln Asn Thr Val Phe Glu Thr Pro Ser
        35                  40                  45

Met Val Ser Val Val Thr Asn Asp Thr Pro Trp Ser Gln Asn Ala Val
    50                  55                  60

Thr Ser Ala Gly Met Leu Lys Gly Val Ala Gly Leu Ser Gln Thr Gly
65                  70                  75                  80

Ala Gly Arg Thr Asn Gly Gln Thr Phe Asn Leu Arg Gly Tyr Asp Lys
                85                  90                  95

Ser Gly Val Leu Val Leu Val Asp Gly Val Arg Gln Leu Ser Asp Met
            100                 105                 110

Ala Lys Ser Ser Gly Thr Tyr Leu Asp Pro Ala Leu Val Lys Arg Ile
        115                 120                 125

Glu Val Val Arg Gly Pro Asn Ser Ser Leu Tyr Gly Ser Gly Gly Leu
    130                 135                 140

Gly Gly Val Val Asp Phe Arg Thr Ala Asp Ala Ala Asp Phe Leu Pro
145                 150                 155                 160

Pro Gly Glu Thr Asn Gly Leu Ser Leu Trp Gly Asn Ile Ala Ser Gly
                165                 170                 175

Asp His Ser Thr Gly Ser Gly Leu Thr Trp Phe Gly Lys Thr Gly Lys
            180                 185                 190

Thr Asp Ala Leu Leu Ser Val Ile Met Arg Lys Arg Gly Asn Ile Tyr
        195                 200                 205

Gln Ser Asp Gly Glu His Ala Pro Asn Lys Glu Lys Pro Ala Ala Leu
    210                 215                 220

Phe Ala Lys Gly Ser Val Gly Ile Thr Asp Ser Asn Lys Ala Gly Ala
225                 230                 235                 240

Ser Leu Arg Leu Tyr Arg Asn Asn Thr Thr Glu Pro Gly Asn Ser Thr
```

245 250 255

Gln Thr His Gly Asp Ser Gly Leu Arg Asp Arg Lys Thr Val Gln Asn
260 265 270

Asp Val Gln Phe Trp Tyr Gln Tyr Ala Pro Val Asp Asn Ser Leu Ile
275 280 285

Asn Val Lys Ser Thr Leu Tyr Leu Ser Asp Ile Thr Ile Lys Thr Asn
290 295 300

Gly His Asn Lys Thr Ala Glu Trp Arg Asn Asn Arg Thr Ser Gly Val
305 310 315 320

Asn Val Val Asn Arg Ser His Thr Leu Ile Phe Pro Gly Ala His Gln
325 330 335

Leu Ser Tyr Gly Ala Glu Tyr Tyr Arg Gln Gln Gln Lys Pro Glu Gly
340 345 350

Ser Ala Thr Leu Tyr Pro Glu Gly Asn Ile Asp Phe Thr Ser Leu Tyr
355 360 365

Phe Gln Asp Glu Met Thr Met Lys Ser Tyr Pro Val Asn Ile Ile Val
370 375 380

Gly Ser Arg Tyr Asp Arg Tyr Lys Ser Phe Asn Pro Arg Ala Gly Glu
385 390 395 400

Leu Lys Ala Glu Arg Leu Ser Pro Arg Ala Ala Ile Ser Val Ser Pro
405 410 415

Thr Asp Trp Leu Met Met Tyr Gly Ser Ile Ser Ser Ala Phe Arg Ala
420 425 430

Pro Thr Met Ala Glu Met Tyr Arg Asp Asp Val His Phe Tyr Arg Lys
435 440 445

Gly Lys Pro Asn Tyr Trp Val Pro Asn Leu Asn Leu Lys Pro Glu Asn
450 455 460

Asn Ile Thr Arg Glu Ile Gly Ala Gly Ile Gln Leu Asp Gly Leu Leu
465 470 475 480

Thr Asp Asn Asp Arg Leu Gln Leu Lys Gly Gly Tyr Phe Gly Thr Asp
485 490 495

Ala Arg Asn Tyr Ile Ala Thr Arg Val Asp Met Lys Arg Met Arg Ser
500 505 510

Tyr Ser Tyr Asn Val Ser Arg Ala Arg Ile Trp Gly Trp Asp Met Gln
515 520 525

Gly Asn Tyr Gln Ser Asp Tyr Val Asp Trp Met Leu Ser Tyr Asn Arg
530 535 540

Thr Glu Ser Met Asp Ala Ser Ser Arg Glu Trp Leu Gly Ser Gly Asn
545 550 555 560

Pro Asp Thr Leu Ile Ser Asp Ile Ser Ile Pro Val Gly His Arg Gly
565 570 575

Val Tyr Ala Gly Trp Arg Ala Glu Leu Ser Ala Ser Ala Thr His Val
580 585 590

Lys Lys Gly Asp Pro His Gln Ala Gly Tyr Thr Ile His Ser Phe Ser
595 600 605

Leu Ser Tyr Lys Pro Val Ser Val Lys Gly Phe Glu Ala Ser Val Thr
610 615 620

Leu Asp Asn Ala Phe Asn Lys Leu Ala Met Asn Gly Lys Gly Val Pro
625 630 635 640

Leu Ser Gly Arg Thr Val Ser Leu Tyr Thr Arg Tyr Gln Trp
645 650

<210> 26
<211> 1376
<212> PRT
<213> Escherichia coli
<400> 26

Met Asn Lys Ile Tyr Ala Leu Lys Tyr Cys Tyr Ile Thr Asn Thr Val
1 5 10 15

Lys Val Val Ser Glu Leu Ala Arg Arg Val Cys Lys Gly Ser Thr Arg

20 25 30

Arg Gly Lys Arg Leu Ser Val Leu Thr Ser Leu Ala Leu Ser Ala Leu
35 40 45

Leu Pro Thr Val Ala Gly Ala Ser Thr Val Gly Gly Asn Asn Pro Tyr
50 55 60

Gln Thr Tyr Arg Asp Phe Ala Glu Asn Lys Gly Gln Phe Gln Ala Gly
65 70 75 80

Ala Thr Asn Ile Pro Ile Phe Asn Asn Lys Gly Glu Leu Val Gly His
85 90 95

Leu Asp Lys Ala Pro Met Val Asp Phe Ser Ser Val Asn Val Ser Ser
100 105 110

Asn Pro Gly Val Ala Thr Leu Ile Asn Pro Gln Tyr Ile Ala Ser Val
115 120 125

Lys His Asn Lys Gly Tyr Gln Ser Val Ser Phe Gly Asp Gly Gln Asn
130 135 140

Ser Tyr His Ile Val Asp Arg Asn Glu His Ser Ser Ser Asp Leu His
145 150 155 160

Thr Pro Arg Leu Asp Lys Leu Val Thr Glu Val Ala Pro Ala Thr Val
165 170 175

Thr Ser Ser Ser Thr Ala Asp Ile Leu Asn Pro Ser Lys Tyr Ser Ala
180 185 190

Phe Tyr Arg Ala Gly Ser Gly Ser Gln Tyr Ile Gln Asp Ser Gln Gly
195 200 205

Lys Arg His Trp Val Thr Gly Gly Tyr Gly Tyr Leu Thr Gly Gly Ile
210 215 220

Leu Pro Thr Ser Phe Phe Tyr His Gly Ser Asp Gly Ile Gln Leu Tyr
225 230 235 240

Met Gly Gly Asn Ile His Asp His Ser Ile Leu Pro Ser Phe Gly Glu
245 250 255

```
Ala Gly Asp Ser Gly Ser Pro Leu Phe Gly Trp Asn Thr Ala Lys Gly
            260                 265                 270

Gln Trp Glu Leu Val Gly Val Tyr Ser Gly Val Gly Gly Gly Thr Asn
        275                 280                 285

Leu Ile Tyr Ser Leu Ile Pro Gln Ser Phe Leu Ser Gln Ile Tyr Ser
    290                 295                 300

Glu Asp Asn Asp Ala Pro Val Phe Phe Asn Ala Ser Ser Gly Ala Pro
305                 310                 315                 320

Leu Gln Trp Lys Phe Asp Ser Ser Thr Gly Thr Gly Ser Leu Lys Gln
                325                 330                 335

Gly Ser Asp Glu Tyr Ala Met His Gly Gln Lys Gly Ser Asp Leu Asn
            340                 345                 350

Ala Gly Lys Asn Leu Thr Phe Leu Gly His Asn Gly Gln Ile Asp Leu
        355                 360                 365

Glu Asn Ser Val Thr Gln Gly Ala Gly Ser Leu Thr Phe Thr Asp Asp
    370                 375                 380

Tyr Thr Val Thr Thr Ser Asn Gly Ser Thr Trp Thr Gly Ala Gly Ile
385                 390                 395                 400

Ile Val Asp Lys Asp Ala Ser Val Asn Trp Gln Val Asn Gly Val Lys
                405                 410                 415

Gly Asp Asn Leu His Lys Ile Gly Glu Gly Thr Leu Val Val Gln Gly
            420                 425                 430

Thr Gly Val Asn Glu Gly Gly Leu Lys Val Gly Asp Gly Thr Val Val
        435                 440                 445

Leu Asn Gln Gln Ala Asp Ser Ser Gly His Val Gln Ala Phe Ser Ser
    450                 455                 460

Val Asn Ile Ala Ser Gly Arg Pro Thr Val Val Leu Ala Asp Asn Gln
465                 470                 475                 480
```

```
Gln Val Asn Pro Asp Asn Ile Ser Trp Gly Tyr Arg Gly Gly Val Leu
                485                 490                 495

Asp Val Asn Gly Asn Asp Leu Thr Phe His Lys Leu Asn Ala Ala Asp
            500                 505                 510

Tyr Gly Ala Thr Leu Gly Asn Ser Ser Asp Lys Thr Ala Asn Ile Thr
        515                 520                 525

Leu Asp Tyr Gln Thr Arg Pro Ala Asp Val Lys Val Asn Glu Trp Ser
    530                 535                 540

Ser Ser Asn Arg Gly Thr Val Gly Ser Leu Tyr Ile Tyr Asn Asn Pro
545                 550                 555                 560

Tyr Thr His Thr Val Asp Tyr Phe Ile Leu Lys Thr Ser Ser Tyr Gly
                565                 570                 575

Trp Phe Pro Thr Gly Gln Val Ser Asn Glu His Trp Glu Tyr Val Gly
            580                 585                 590

His Asp Gln Asn Ser Ala Gln Ala Leu Leu Ala Asn Arg Ile Asn Asn
        595                 600                 605

Lys Gly Tyr Leu Tyr His Gly Lys Leu Leu Gly Asn Ile Asn Phe Ser
    610                 615                 620

Asn Lys Ala Thr Pro Gly Thr Thr Gly Ala Leu Val Met Asp Gly Ser
625                 630                 635                 640

Ala Asn Met Ser Gly Thr Phe Thr Gln Glu Asn Gly Arg Leu Thr Ile
                645                 650                 655

Gln Gly His Pro Val Ile His Ala Ser Thr Ser Gln Ser Ile Ala Asn
            660                 665                 670

Thr Val Ser Ser Leu Gly Asp Asn Ser Val Leu Thr Gln Pro Thr Ser
        675                 680                 685

Phe Thr Gln Asp Asp Trp Glu Asn Arg Thr Phe Ser Phe Gly Ser Leu
    690                 695                 700
```

Val Leu Lys Asp Thr Asp Phe Gly Leu Gly Arg Asn Ala Thr Leu Asn
705 710 715 720

Thr Thr Ile Gln Ala Asp Asn Ser Ser Val Thr Leu Gly Asp Ser Arg
725 730 735

Val Phe Ile Asp Lys Lys Asp Gly Gln Gly Thr Ala Phe Thr Leu Glu
740 745 750

Glu Gly Thr Ser Val Ala Thr Lys Asp Ala Asp Lys Ser Val Phe Asn
755 760 765

Gly Thr Val Asn Leu Asp Asn Gln Ser Val Leu Asn Ile Asn Glu Ile
770 775 780

Phe Asn Gly Gly Ile Gln Ala Asn Asn Ser Thr Val Asn Ile Ser Ser
785 790 795 800

Asp Ser Ala Val Leu Glu Asn Ser Thr Leu Thr Ser Thr Ala Leu Asn
805 810 815

Leu Asn Lys Gly Ala Asn Val Leu Ala Ser Gln Ser Phe Val Ser Asp
820 825 830

Gly Pro Val Asn Ile Ser Asp Ala Thr Leu Ser Leu Asn Ser Arg Pro
835 840 845

Asp Glu Val Ser His Thr Leu Leu Pro Val Tyr Asp Tyr Ala Gly Ser
850 855 860

Trp Asn Leu Lys Gly Asp Asp Ala Arg Leu Asn Val Gly Pro Tyr Ser
865 870 875 880

Met Leu Ser Gly Asn Ile Asn Val Gln Asp Lys Gly Thr Val Thr Leu
885 890 895

Gly Gly Glu Gly Glu Leu Ser Pro Asp Leu Thr Leu Gln Asn Gln Met
900 905 910

Leu Tyr Ser Leu Phe Asn Gly Tyr Arg Asn Thr Trp Ser Gly Ser Leu
915 920 925

Asn Ala Pro Asp Ala Thr Val Ser Met Thr Asp Thr Gln Trp Ser Met

930 935 940

Asn Gly Asn Ser Thr Ala Gly Asn Met Lys Leu Asn Arg Thr Ile Val
945 950 955 960

Gly Phe Asn Gly Gly Thr Ser Ser Phe Thr Thr Leu Thr Thr Asp Asn
965 970 975

Leu Asp Ala Val Gln Ser Ala Phe Val Met Arg Thr Asp Leu Asn Lys
980 985 990

Ala Asp Lys Leu Val Ile Asn Lys Ser Ala Thr Gly His Asp Asn Ser
995 1000 1005

Ilė Trp Val Asn Phe Leu Lys Lys Pro Ser Asp Lys Asp Thr Leu
1010 1015 1020

Asp Ile Pro Leu Val Ser Ala Pro Glu Ala Thr Ala Asp Asn Leu
1025 1030 1035

Phe Arg Ala Ser Thr Arg Val Val Gly Phe Ser Asp Val Thr Pro
1040 1045 1050

Thr Leu Ser Val Arg Lys Glu Asp Gly Lys Lys Glu Trp Val Leu
1055 1060 1065

Asp Gly Tyr Gln Val Ala Arg Asn Asp Gly Gln Gly Lys Ala Ala
1070 1075 1080

Ala Thr Phe Met His Ile Ser Tyr Asn Asn Phe Ile Thr Glu Val
1085 1090 1095

Asn Asn Leu Asn Lys Arg Met Gly Asp Leu Arg Asp Ile Asn Gly
1100 1105 1110

Glu Ala Gly Thr Trp Val Arg Leu Leu Asn Gly Ser Gly Ser Ala
1115 1120 1125

Asp Gly Gly Phe Thr Asp His Tyr Thr Leu Leu Gln Met Gly Ala
1130 1135 1140

Asp Arg Lys His Glu Leu Gly Ser Met Asp Leu Phe Thr Gly Val
1145 1150 1155

Met Ala Thr Tyr Thr Asp Thr Asp Ala Ser Ala Gly Leu Tyr Ser
1160 1165 1170

Gly Lys Thr Lys Ser Trp Gly Gly Gly Phe Tyr Ala Ser Gly Leu
1175 1180 1185

Phe Arg Ser Gly Ala Tyr Phe Asp Leu Ile Ala Lys Tyr Ile His
1190 1195 1200

Asn Glu Asn Lys Tyr Asp Leu Asn Phe Ala Gly Ala Gly Lys Gln
1205 1210 1215

Asn Phe Arg Ser His Ser Leu Tyr Ala Gly Ala Glu Val Gly Tyr
1220 1225 1230

Arg Tyr His Leu Thr Asp Thr Thr Phe Val Glu Pro Gln Ala Glu
1235 1240 1245

Leu Val Trp Gly Arg Leu Gln Gly Gln Thr Phe Asn Trp Asn Asp
1250 1255 1260

Ser Gly Met Asp Val Ser Met Arg Arg Asn Ser Val Asn Pro Leu
1265 1270 1275

Val Gly Arg Thr Gly Val Val Ser Gly Lys Thr Phe Ser Gly Lys
1280 1285 1290

Asp Trp Ser Leu Thr Ala Arg Ala Gly Leu His Tyr Glu Phe Asp
1295 1300 1305

Leu Thr Asp Ser Ala Asp Val His Leu Lys Asp Ala Ala Gly Glu
1310 1315 1320

His Gln Ile Asn Gly Arg Lys Asp Gly Arg Met Leu Tyr Gly Val
1325 1330 1335

Gly Leu Asn Ala Arg Phe Gly Asp Asn Thr Arg Leu Gly Leu Glu
1340 1345 1350

Val Glu Arg Ser Ala Phe Gly Lys Tyr Asn Thr Asp Asp Ala Ile
1355 1360 1365

Asn Ala Asn Ile Arg Tyr Ser Phe
1370 1375

<210> 27
<211> 349
<212> PRT
<213> Escherichia coli
<400> 27

Met Ile Thr Leu Phe Arg Leu Leu Ala Ile Leu Cys Leu Phe Phe Asn
1 5 10 15

Val Ser Ala Phe Ala Val Asp Cys Tyr Gln Asp Gly Tyr Arg Gly Thr
20 25 30

Thr Leu Ile Asn Gly Asp Leu Pro Thr Phe Lys Ile Pro Glu Asn Ala
35 40 45

Gln Pro Gly Gln Lys Ile Trp Glu Ser Gly Asp Ile Asn Ile Thr Val
50 55 60

Tyr Cys Asp Asn Ala Pro Gly Trp Ser Ser Asn Asn Pro Ser Glu Asn
65 70 75 80

Val Tyr Ala Trp Ile Lys Leu Pro Gln Ile Asn Ser Ala Asp Met Leu
85 90 95

Asn Asn Pro Tyr Leu Thr Phe Gly Val Thr Tyr Asn Gly Val Asp Tyr
100 105 110

Glu Gly Thr Asn Glu Lys Ile Asp Thr His Ala Cys Leu Asp Lys Tyr
115 120 125

Glu Gln Tyr Tyr Asn Gly Tyr Tyr His Asp Pro Val Cys Asn Gly Ser
130 135 140

Thr Leu Gln Lys Asn Val Thr Phe Asn Ala His Phe Arg Val Tyr Val
145 150 155 160

Lys Phe Lys Ser Arg Pro Ala Gly Asp Gln Thr Val Asn Phe Gly Thr
165 170 175

Val Asn Val Leu Gln Phe Asp Gly Glu Gly Gly Ala Asn Met Ala Pro
180 185 190

Asn Ala Lys Asn Leu Arg Tyr Ala Ile Thr Gly Leu Asp Asn Ile Ser
195 200 205

Phe Leu Asp Cys Ser Val Asp Val Arg Ile Ser Pro Glu Ser Gln Ile
210 215 220

Val Asn Phe Gly Gln Ile Ala Ala Asn Ser Ile Ala Thr Phe Pro Pro
225 230 235 240

Lys Ala Ala Phe Ser Val Ser Thr Ile Lys Asp Ile Ala Ser Asp Cys
245 250 255

Thr Glu Gln Phe Asp Val Ala Thr Ser Phe Phe Thr Ser Asp Thr Leu
260 265 270

Tyr Asp Asn Thr His Leu Glu Ile Gly Asn Gly Leu Leu Met Arg Ile
275 280 285

Thr Asp Gln Lys Thr Gln Glu Asp Ile Lys Phe Asn Gln Phe Lys Leu
290 295 300

Phe Ser Thr Tyr Ile Pro Gly Gln Ser Ala Ala Met Ala Thr Arg Asp
305 310 315 320

Tyr Gln Ala Glu Leu Thr Gln Lys Pro Gly Glu Pro Leu Val Tyr Gly
325 330 335

Pro Phe Gln Lys Asp Leu Ile Val Lys Ile Asn Tyr His
340 345

<210> 28
<211> 840
<212> PRT
<213> Escherichia coli
<400> 28

Met Asn Asn Lys Asn Thr Phe Ser Arg Asp Lys Leu Ser His Ala Ile
1 5 10 15

Lys Asn Ala Leu Ser Gly Val Val Cys Ser Leu Leu Phe Val Leu Pro
20 25 30

Val His Ala Val Glu Phe Asn Val Asp Met Ile Asp Ala Glu Asp Arg

35 40 45

Glu Asn Ile Asp Ile Ser Arg Phe Glu Lys Lys Gly Tyr Ile Pro Pro
50 55 60

Gly Arg Tyr Leu Val Arg Val Gln Ile Asn Lys Asn Met Leu Pro Gln
65 70 75 80

Thr Leu Ile Leu Glu Trp Val Lys Ala Asp Asn Glu Ser Gly Ser Leu
85 90 95

Leu Cys Leu Thr Lys Glu Asn Leu Thr Asn Phe Gly Leu Asn Thr Glu
100 105 110

Phe Ile Glu Ser Leu Gln Asn Ile Ala Gly Ser Glu Cys Leu Asp Leu
115 120 125

Ser Gln Arg Gln Glu Leu Thr Thr Arg Leu Asp Lys Ala Thr Met Ile
130 135 140

Leu Ser Leu Ser Val Pro Gln Ala Trp Leu Lys Tyr Gln Ala Thr Asn
145 150 155 160

Trp Thr Pro Pro Glu Phe Trp Asp Thr Gly Ile Thr Gly Phe Ile Leu
165 170 175

Asp Tyr Asn Val Tyr Ala Ser Gln Tyr Ala Pro His His Gly Asp Ser
180 185 190

Thr Gln Asn Val Ser Ser Tyr Gly Thr Leu Gly Phe Asn Leu Gly Ala
195 200 205

Trp Arg Leu Arg Ser Asp Tyr Gln Tyr Asn Gln Asn Phe Ala Asp Gly
210 215 220

Arg Ser Val Asn Arg Asp Ser Glu Phe Ala Arg Thr Tyr Leu Phe Arg
225 230 235 240

Pro Ile Pro Ser Trp Ser Ser Lys Phe Thr Met Gly Gln Tyr Asp Leu
245 250 255

Ser Ser Asn Leu Tyr Asp Thr Phe His Phe Thr Gly Ala Ser Leu Glu
260 265 270

```
Ser Asp Glu Ser Met Leu Pro Pro Asp Leu Gln Gly Tyr Ala Pro Gln
        275                 280                 285

Ile Thr Gly Ile Ala Gln Thr Asn Ala Lys Val Thr Val Ala Gln Asn
    290                 295                 300

Gly Arg Val Leu Tyr Gln Thr Thr Val Ala Pro Gly Pro Phe Thr Ile
305                 310                 315                 320

Ser Asp Leu Gly Gln Ser Phe Gln Gly Gln Leu Asp Val Thr Val Glu
                325                 330                 335

Glu Glu Asp Gly Arg Thr Ser Thr Phe Gln Val Gly Ser Ala Ser Ile
            340                 345                 350

Pro Tyr Leu Thr Arg Lys Gly Gln Val Arg Tyr Lys Thr Ser Leu Gly
        355                 360                 365

Lys Pro Thr Ser Val Gly His Asn Asp Ile Asn Asn Pro Phe Phe Trp
    370                 375                 380

Thr Ala Glu Ala Ser Trp Gly Trp Leu Asn Asn Val Ser Leu Tyr Gly
385                 390                 395                 400

Gly Gly Met Phe Thr Ala Asp Asp Tyr Gln Ala Ile Thr Thr Gly Ile
                405                 410                 415

Gly Phe Asn Leu Asn Gln Phe Gly Ser Leu Ser Phe Asp Val Thr Gly
            420                 425                 430

Ala Asp Ala Ser Leu Gln Gln Gln Asn Ser Gly Asn Leu Arg Gly Tyr
        435                 440                 445

Ser Tyr Arg Phe Asn Tyr Ala Lys His Phe Glu Ser Thr Gly Ser Gln
    450                 455                 460

Ile Thr Phe Ala Gly Tyr Arg Phe Ser Asp Lys Asp Tyr Val Ser Met
465                 470                 475                 480

Ser Glu Tyr Leu Ser Ser Arg Asn Gly Asp Glu Ser Ile Asp Asn Glu
                485                 490                 495
```

Lys Glu Ser Tyr Val Ile Ser Leu Asn Gln Tyr Phe Glu Thr Leu Glu
500 505 510

Leu Asn Ser Tyr Leu Asn Val Thr Arg Asn Thr Tyr Trp Asp Ser Ala
515 520 525

Ser Asn Thr Asn Tyr Ser Val Ser Val Ser Lys Asn Phe Asp Ile Gly
530 535 540

Asp Phe Lys Gly Ile Ser Ala Ser Leu Ala Val Ser Arg Ile Arg Trp
545 550 555 560

Asp Asp Asp Glu Glu Asn Gln Tyr Tyr Phe Ser Phe Ser Leu Pro Leu
565 570 575

Gln Gln Asn Arg Asn Ile Ser Tyr Ser Met Gln Arg Thr Gly Ser Ser
580 585 590

Asn Thr Ser Gln Met Ile Ser Trp Tyr Asp Ser Ser Asp Arg Asn Asn
595 600 605

Ile Trp Asn Ile Ser Ala Ser Ala Thr Asp Asp Asn Ile Arg Asp Gly
610 615 620

Glu Pro Thr Leu Arg Gly Ser Tyr Gln His Tyr Ser Pro Trp Gly Arg
625 630 635 640

Leu Asn Ile Asn Gly Ser Val Gln Pro Asn Gln Tyr Asn Ser Val Thr
645 650 655

Ala Gly Trp Tyr Gly Ser Leu Thr Ala Thr Arg His Gly Val Ala Leu
660 665 670

His Asp Tyr Ser Tyr Gly Asp Asn Ala Arg Met Met Val Asp Thr Asp
675 680 685

Gly Ile Ser Gly Ile Glu Ile Asn Ser Asn Arg Thr Val Thr Asn Gly
690 695 700

Leu Gly Ile Ala Val Ile Pro Ser Leu Ser Asn Tyr Thr Thr Ser Met
705 710 715 720

Leu Arg Val Asn Asn Asn Asp Leu Pro Glu Gly Val Asp Val Glu Asn
725 730 735

Ser Val Ile Arg Thr Thr Leu Thr Gln Gly Ala Ile Gly Tyr Ala Lys
740 745 750

Leu Asn Ala Thr Thr Gly Tyr Gln Ile Val Gly Val Ile Arg Gln Glu
755 760 765

Asn Gly Arg Phe Pro Pro Leu Gly Val Asn Val Thr Asp Lys Ala Thr
770 775 780

Gly Lys Asp Val Gly Leu Val Ala Glu Asp Gly Phe Val Tyr Leu Ser
785 790 795 800

Gly Ile Gln Glu Asn Ser Ile Leu His Leu Thr Trp Gly Asp Asn Thr
805 810 815

Cys Glu Val Thr Pro Pro Asn Gln Ser Asn Ile Ser Glu Ser Ala Ile
820 825 830

Ile Leu Pro Cys Lys Thr Val Lys
835 840

<210> 29
<211> 169
<212> PRT
<213> Escherichia coli
<400> 29

Leu Met Asn Thr Lys Gln Ser Val Ala Gln Leu Ala Val Pro His Arg
1 5 10 15

Lys Arg Leu Ser Ser Thr Met Val Val Ala Leu Leu Leu Cys Val Val
20 25 30

Ala Gly Ala Val Met Ile Asn Ala Ala Asp Phe Pro Ala Thr Ala Ile
35 40 45

Glu Thr Asp Pro Gly Ala Ser Ala Phe Pro Thr Phe Tyr Ala Cys Ala
50 55 60

Leu Ile Val Leu Ala Val Leu Leu Val Ile Arg Asp Leu Leu Gln Ala
65 70 75 80

Lys Pro Ala Ser Cys Ala Asn Ala Gln Glu Lys Pro Ala Phe Arg Lys
85 90 95

Thr Ala Thr Gly Ile Ala Ala Thr Ala Phe Tyr Ile Val Ala Met Ser
100 105 110

Tyr Cys Gly Tyr Leu Ile Thr Thr Pro Val Phe Leu Ile Val Ile Met
115 120 125

Thr Leu Met Gly Tyr Arg Arg Trp Val Leu Thr Pro Gly Ile Ala Leu
130 135 140

Leu Leu Thr Ala Ile Leu Trp Leu Leu Phe Val Glu Ala Leu Gln Val
145 150 155 160

Pro Leu Pro Val Gly Thr Phe Phe Glu
165

<210> 30
<211> 311
<212> PRT
<213> *Escherichia coli*
<400> 30

Met Val Leu Leu Ala Gly Ala Ala Leu Ser Ile Ala Pro Val Gln Ala
1 5 10 15

Ala Ser Tyr Pro Thr Lys Gln Ile Glu Leu Val Val Pro Tyr Ala Ala
20 25 30

Gly Gly Gly Thr Asp Leu Val Ala Arg Ala Phe Ala Asp Ala Ala Lys
35 40 45

Asn His Leu Pro Val Ser Ile Gly Val Ile Asn Lys Pro Gly Gly Gly
50 55 60

Gly Ala Ile Gly Leu Ser Glu Ile Ala Ala Ala Arg Pro Asn Gly Tyr
65 70 75 80

Lys Ile Gly Leu Gly Thr Val Glu Leu Thr Thr Leu Pro Ser Leu Gly
85 90 95

Met Val Arg Phe Lys Thr Ser Asp Phe Lys Pro Ile Ala Arg Leu Asn
100 105 110

```
Ala Asp Pro Ala Ala Ile Thr Val Arg Ala Asp Ala Pro Trp Asn Ser
        115                 120                 125

Tyr Glu Glu Phe Met Ala Tyr Ser Lys Ala Asn Pro Gly Lys Val Arg
    130                 135                 140

Ile Gly Asn Ser Gly Thr Gly Ala Ile Trp His Leu Ala Ala Ala Ala
145                 150                 155                 160

Leu Glu Asp Lys Thr Gly Thr Lys Phe Ser His Val Pro Tyr Asp Gly
                165                 170                 175

Ala Ala Pro Ala Ile Thr Gly Leu Leu Gly Gly His Ile Glu Ala Val
            180                 185                 190

Ser Val Ser Pro Gly Glu Val Ile Asn His Val Asn Gly Gly Lys Leu
        195                 200                 205

Lys Thr Leu Val Val Met Ala Asp Glu Arg Met Lys Thr Met Pro Asp
    210                 215                 220

Val Pro Thr Leu Lys Glu Lys Gly Val Asp Leu Ser Ile Gly Thr Trp
225                 230                 235                 240

Arg Gly Leu Ile Val Ser Gln Lys Thr Pro Gln Asp Val Val Asp Val
                245                 250                 255

Leu Ala Lys Ala Ala Lys Glu Thr Ala Glu Glu Pro Ala Phe Gln Asp
            260                 265                 270

Ala Leu Gln Lys Leu Asn Leu Asn Tyr Ala Trp Leu Asp Ala Ala Ser
        275                 280                 285

Phe Gln Thr Gln Ile Ser Glu Gln Glu Lys Tyr Phe Asp Glu Leu Leu
    290                 295                 300

Thr Arg Leu Gly Leu Lys Lys
305                 310
```

<210> 31
<211> 722
<212> PRT

<213> Escherichia coli
<400> 31

Met Leu Arg Trp Lys Arg Cys Ile Ile Leu Thr Phe Ile Ser Gly Ala
1 5 10 15

Ala Phe Ala Ala Pro Glu Ile Asn Val Lys Gln Asn Glu Ser Leu Pro
20 25 30

Asp Leu Gly Ser Gln Ala Ala Gln Gln Asp Glu Gln Thr Asn Lys Gly
35 40 45

Lys Ser Leu Lys Glu Arg Gly Ala Asp Tyr Val Ile Asn Ser Ala Thr
50 55 60

Gln Gly Phe Glu Asn Leu Thr Pro Glu Ala Leu Glu Ser Gln Ala Arg
65 70 75 80

Ser Tyr Leu Gln Ser Gln Ile Thr Ser Thr Ala Gln Ser Tyr Ile Glu
85 90 95

Asp Thr Leu Ser Pro Tyr Gly Lys Val Arg Leu Asn Leu Ser Ile Gly
100 105 110

Gln Gly Gly Asp Leu Asp Gly Ser Ser Ile Asp Tyr Phe Val Pro Trp
115 120 125

Tyr Asp Asn Gln Thr Thr Val Tyr Phe Ser Gln Phe Ser Ala Gln Arg
130 135 140

Lys Glu Asp Arg Thr Ile Gly Asn Ile Gly Leu Gly Val Arg Tyr Asn
145 150 155 160

Phe Asp Lys Tyr Leu Leu Gly Gly Asn Ile Phe Tyr Asp Tyr Asp Phe
165 170 175

Thr Arg Gly His Arg Arg Leu Gly Leu Gly Ala Glu Ala Trp Thr Asp
180 185 190

Tyr Leu Lys Phe Ser Gly Asn Tyr Tyr His Pro Leu Ser Asp Trp Lys
195 200 205

Asp Ser Glu Asp Phe Asp Phe Tyr Glu Glu Arg Pro Ala Arg Gly Trp
210 215 220

```
Asp Ile Arg Ala Glu Val Trp Leu Pro Ser Tyr Pro Gln Leu Gly Gly
225                 230                 235                 240

Lys Ile Val Phe Glu Gln Tyr Tyr Gly Asp Glu Val Ala Leu Phe Gly
                245                 250                 255

Thr Asp Asn Leu Glu Lys Asp Pro Tyr Ala Val Thr Leu Gly Leu Asn
            260                 265                 270

Tyr Gln Pro Val Pro Leu Leu Thr Val Gly Thr Asp Tyr Lys Ala Gly
        275                 280                 285

Thr Gly Asp Asn Ser Asp Val Ser Ile Asn Ala Thr Leu Asn Tyr Gln
    290                 295                 300

Phe Gly Val Pro Leu Lys Asp Gln Leu Asp Ser Asp Lys Val Lys Ala
305                 310                 315                 320

Ala His Ser Leu Met Gly Ser Arg Leu Asp Phe Val Glu Arg Asn Asn
                325                 330                 335

Phe Ile Val Leu Glu Tyr Lys Glu Lys Asp Pro Leu Asp Val Thr Leu
            340                 345                 350

Trp Leu Lys Ala Asp Ala Thr Asn Glu His Pro Glu Cys Val Ile Lys
        355                 360                 365

Asp Thr Pro Glu Ala Ala Val Gly Leu Glu Lys Cys Lys Trp Thr Ile
    370                 375                 380

Asn Ala Leu Ile Asn His His Tyr Lys Ile Val Ala Ala Ser Trp Gln
385                 390                 395                 400

Ala Lys Asn Asn Ala Ala Arg Thr Leu Val Met Pro Val Ile Lys Glu
                405                 410                 415

Asn Thr Leu Thr Glu Gly Asn Asn Asn His Trp Asn Leu Val Leu Pro
            420                 425                 430

Ala Trp Gln Tyr Ser Ser Asp Gln Ala Glu Gln Glu Lys Leu Asn Thr
        435                 440                 445
```

```
Trp Arg Val Arg Leu Ala Leu Glu Asp Glu Lys Gly Asn Arg Gln Asn
    450                 455                 460

Ser Gly Val Val Glu Ile Thr Val Gln Gln Asp Arg Lys Ile Glu Leu
465                 470                 475                 480

Ile Val Asn Asn Ile Ala Asn Pro Glu Glu Asn Asn His Ser His Glu
                485                 490                 495

Ala Ser Ala Gln Ala Asp Gly Val Asp Gly Val Val Met Asp Leu Asp
            500                 505                 510

Val Thr Asp Ser Phe Gly Asp Asn Thr Asp Arg Asn Gly Asp Ala Leu
        515                 520                 525

Pro Glu Asp Asn Leu Thr Pro Gln Leu Tyr Asp Ala Gln Asp Lys Arg
    530                 535                 540

Val Thr Leu Thr Asn Lys Pro Cys Ser Thr Asp Asn Pro Cys Val Phe
545                 550                 555                 560

Ile Ala Lys Gln Asp Lys Glu Lys Gly Thr Val Thr Leu Ser Ser Thr
                565                 570                 575

Leu Pro Gly Thr Tyr Arg Trp Lys Ala Lys Ala Ala Pro Tyr Asp Asp
            580                 585                 590

Ser Asn Tyr Val Asp Val Thr Phe Leu Gly Ala Glu Ile Gly Gly Leu
        595                 600                 605

Asn Ala Phe Ile Tyr Arg Val Gly Ala Ala Lys Pro Ser Asn Leu Ile
    610                 615                 620

Gly Lys Asp Lys Glu Pro Leu Pro Ser Thr Thr Phe Ile Asp Leu Phe
625                 630                 635                 640

Tyr Gly Ala Thr Thr Ile Lys Thr Val Ser Ser Ser Arg Ser Lys Asn
                645                 650                 655

Leu Thr Lys Arg Trp Cys Ser Thr Thr Thr Ser Gly Asn Leu Pro Ala
            660                 665                 670
```

```
Arg Ala Ser Met Val Ser Gly Cys Thr Gly Glu His Ser Asn Glu Asp
        675                 680                 685

Ile Val Ile Pro Ala Thr Asn Arg Glu Ala Ala Gln Thr Tyr Gly Ala
    690                 695                 700

Gln Ala Gly Asp Gly Leu Gln Gly Tyr Gly Leu Arg Val Leu Tyr Thr
705                 710                 715                 720

Lys Lys
```

<210> 32
<211> 319
<212> PRT
<213> Escherichia coli
<400> 32

```
Met Lys Gln Asp Lys Arg Arg Gly Leu Thr Arg Ile Ala Leu Ala Leu
1               5                   10                  15

Ala Leu Ala Gly Tyr Cys Val Ala Pro Val Ala Leu Ala Glu Asp Ser
            20                  25                  30

Ala Trp Val Asp Ser Gly Glu Thr Asn Ile Phe Gln Gly Thr Ile Pro
        35                  40                  45

Trp Leu Tyr Ser Glu Gly Gly Ser Ala Thr Thr Asp Ala Asp Arg Val
    50                  55                  60

Thr Leu Thr Ser Asp Leu Lys Gly Ala Arg Pro Gln Gly Met Lys Arg
65                  70                  75                  80

Thr Ser Val Phe Thr Arg Val Ile Asn Ile Gly Asp Thr Glu Gly Asp
                85                  90                  95

Val Asp Leu Gly Gly Leu Gly Asp Asn Ala Lys Thr Ile Asp Thr Ile
            100                 105                 110

Arg Trp Met Ser Tyr Lys Asp Ala Gln Gly Gly Asp Pro Lys Glu Leu
        115                 120                 125

Ala Thr Lys Val Thr Ser Tyr Thr Leu Thr Asp Ala Asp Arg Gly Arg
    130                 135                 140
```

Tyr Ile Gly Ile Glu Ile Thr Pro Thr Thr Gln Thr Gly Thr Pro Asn
145 150 155 160

Val Gly Thr Ala Leu His Leu Tyr Asp Val Ser Thr Ala Ser Gly Gly
165 170 175

Gly Ser Asp Ser Asp Asn Val Ala Pro Gly Pro Val Val Asn Gln Asn
180 185 190

Leu Lys Val Ala Ile Phe Val Asp Gly Thr Ser Ile Asn Leu Ile Asn
195 200 205

Gly Ser Thr Pro Ile Glu Leu Gly Lys Thr Tyr Val Ala Lys Leu Tyr
210 215 220

Ser Asp Glu Asn Lys Asn Gly Lys Phe Asp Ala Gly Thr Asp Ala Asp
225 230 235 240

Val Thr Ala Asn Tyr Asp Phe Arg Trp Val Leu Ser Gly Ser Ser Gln
245 250 255

Gln Leu Gly Thr Ser Gly Gly Ile Val Asn Ser Ser Phe Asp Asn Asn
260 265 270

Asn Leu Val Ile Pro Ala Thr Asn Asp Glu Ala Arg Thr Asn Leu Asn
275 280 285

Gly Pro Ala Arg Asp Gly Lys Glu Ala Leu Ser Ile Pro Thr Asn Gly
290 295 300

Asp Gly Val Gln Gly Tyr Lys Leu His Ile Ile Tyr Lys His Lys
305 310 315

<210> 33
<211> 629
<212> PRT
<213> Escherichia coli
<400> 33

Met Lys Lys Val Leu Thr Leu Ser Leu Leu Ala Leu Cys Val Ser His
1 5 10 15

Ser Ala Val Ala Ala Asn Tyr Thr Phe Asn Asn Asp Asn Ile Ala Leu
20 25 30

Ser Phe Asp Asp Thr Asn Ser Thr Ile Val Leu Lys Asp Arg Arg Thr
35 40 45

Asn His Pro Ile Thr Pro Gln Glu Leu Phe Phe Leu Thr Leu Pro Asp
50 55 60

Glu Thr Lys Ile His Thr Ala Asp Phe Lys Ile Lys His Ile Lys Lys
65 70 75 80

Gln Asp Asn Ala Ile Val Ile Asp Phe Thr Arg Pro Asp Phe Asn Val
85 90 95

Thr Val Gln Leu Asn Leu Val Lys Gly Lys Tyr Ala Ser Ile Asp Tyr
100 105 110

Thr Ile Ala Ala Val Gly Gln Pro Arg Asp Val Ala Lys Ile Thr Phe
115 120 125

Phe Pro Thr Lys Lys Gln Phe Gln Ala Pro Tyr Val Asp Gly Ala Ile
130 135 140

Thr Ser Ser Pro Ile Ile Ala Asp Ser Phe Phe Ile Leu Pro Asn Lys
145 150 155 160

Pro Ile Val Asn Thr Tyr Ala Tyr Glu Ala Thr Thr Asn Leu Asn Val
165 170 175

Glu Leu Lys Thr Pro Ile Gln Pro Glu Thr Pro Val Ser Phe Thr Thr
180 185 190

Trp Phe Gly Thr Phe Pro Glu Thr Ser Gln Leu Arg Arg Ser Val Asn
195 200 205

Gln Phe Ile Asn Ala Val Arg Pro Arg Pro Tyr Lys Pro Tyr Leu His
210 215 220

Tyr Asn Ser Trp Met Asp Ile Gly Phe Phe Thr Pro Tyr Thr Glu Gln
225 230 235 240

Asp Val Leu Gly Arg Met Asp Glu Trp Asn Lys Glu Phe Ile Ser Gly
245 250 255

```
Arg Gly Val Ala Leu Asp Ala Phe Leu Leu Asp Asp Gly Trp Asp Asp
            260                 265                 270

Leu Thr Gly Arg Trp Leu Phe Gly Pro Ala Phe Ser Asn Gly Phe Ser
        275                 280                 285

Lys Val Arg Glu Lys Ala Asp Ser Leu His Ser Ser Val Gly Leu Trp
    290                 295                 300

Leu Ser Pro Trp Gly Gly Tyr Asn Lys Pro Gln Arg Arg Ser Arg Phe
305                 310                 315                 320

Ala Cys Lys Arg Val Trp Val Arg Asn Arg Gly Arg Gln Ala Gly Ala
                325                 330                 335

Phe Gly Ser Glu Leu Leu Lys Asn Phe Asn Glu Gln Ile Ile Asn Leu
            340                 345                 350

Ile Lys Asn Glu His Ile Thr Ser Phe Lys Leu Asp Gly Met Gly Asn
        355                 360                 365

Ala Ser Ser His Ile Lys Gly Ser Pro Phe Ala Ser Asp Phe Asp Ala
    370                 375                 380

Ser Ile Ala Leu Leu His Asn Met Arg Arg Ala Asn Pro Asn Leu Phe
385                 390                 395                 400

Ile Asn Leu Thr Thr Gly Thr Asn Ala Ser Pro Ser Trp Leu Phe Tyr
                405                 410                 415

Ala Asp Ser Ile Trp Arg Gln Gly Asp Asp Ile Asn Leu Tyr Gly Pro
            420                 425                 430

Gly Thr Pro Val Gln Gln Trp Ile Thr Tyr Arg Asp Ala Glu Thr Tyr
        435                 440                 445

Arg Ser Ile Val Arg Lys Gly Pro Leu Phe Pro Leu Asn Ser Leu Met
    450                 455                 460

Tyr His Gly Ile Val Ser Ala Glu Asn Ala Tyr Tyr Gly Leu Glu Lys
465                 470                 475                 480
```

Val Gln Thr Asp Ser Asp Phe Ala Asp Gln Val Trp Ser Tyr Phe Ala
485 490 495

Thr Gly Thr Gln Leu Gln Glu Leu Tyr Ile Thr Pro Ser Met Leu Asn
500 505 510

Lys Val Lys Trp Asp Thr Leu Ala Lys Ala Ala Lys Trp Ser Lys Glu
515 520 525

Asn Ala Ser Val Leu Val Asp Thr His Trp Ile Gly Gly Asp Pro Thr
530 535 540

Ala Leu Ala Val Tyr Gly Trp Ala Ser Trp Ser Lys Asp Lys Ala Ile
545 550 555 560

Leu Gly Leu Arg Asn Pro Ser Asp Lys Pro Gln Thr Tyr Tyr Leu Asp
565 570 575

Leu Ala Lys Asp Phe Glu Ile Pro Ala Gly Asn Ala Ala Gln Phe Ser
580 585 590

Leu Lys Ala Val Tyr Gly Ser Asn Lys Thr Val Pro Val Glu Tyr Lys
595 600 605

Asn Ala Thr Val Ile Thr Leu Gln Pro Leu Glu Thr Leu Val Phe Glu
610 615 620

Ala Val Thr Ile Asn
625

<210> 34
<211> 1778
<212> PRT
<213> Escherichia coli
<400> 34

Met Asn Lys Ile Phe Lys Val Ile Trp Asn Pro Ala Thr Gly Ser Tyr
1 5 10 15

Thr Val Ala Ser Glu Thr Ala Lys Ser Arg Gly Lys Lys Ser Gly Arg
20 25 30

Ser Lys Leu Leu Ile Ser Ala Leu Val Ala Gly Gly Leu Leu Ser Ser
35 40 45

Phe Gly Ala Ser Ala Asp Asn Tyr Thr Gly Gln Pro Thr Asp Tyr Gly
50 55 60

Asp Gly Ser Ala Gly Asp Gly Trp Val Ala Ile Gly Lys Gly Ala Lys
65 70 75 80

Ala Asn Thr Phe Met Asn Thr Ser Gly Ala Ser Thr Ala Leu Gly Tyr
85 90 95

Asp Ala Ile Ala Glu Gly Glu Tyr Ser Ser Ala Ile Gly Ser Lys Thr
100 105 110

Leu Ala Thr Gly Gly Ala Ser Met Ala Phe Gly Val Ser Ala Lys Ala
115 120 125

Met Gly Asp Arg Ser Val Ala Leu Gly Ala Ser Ser Val Ala Asn Gly
130 135 140

Asp Arg Ser Met Ala Phe Gly Arg Tyr Ala Lys Thr Asn Gly Phe Thr
145 150 155 160

Ser Leu Ala Ile Gly Asp Ser Ser Leu Ala Asp Gly Glu Lys Thr Ile
165 170 175

Ala Leu Gly Asn Thr Ala Lys Ala Tyr Glu Ile Met Ser Ile Ala Leu
180 185 190

Gly Asp Asn Ala Asn Ala Ser Lys Glu Tyr Ala Met Ala Leu Gly Ala
195 200 205

Ser Ser Lys Ala Gly Gly Ala Asp Ser Leu Ala Phe Gly Arg Lys Ser
210 215 220

Thr Ala Asn Ser Thr Gly Ser Leu Ala Ile Gly Ala Asp Ser Ser Ser
225 230 235 240

Ser Asn Asp Asn Ala Ile Ala Ile Gly Asn Lys Thr Gln Ala Leu Gly
245 250 255

Val Asn Ser Met Ala Leu Gly Asn Ala Ser Gln Ala Ser Gly Glu Ser
260 265 270

Ser Ile Ala Leu Gly Asn Thr Ser Glu Ala Ser Glu Gln Asn Ala Ile
275 280 285

Ala Leu Gly Gln Gly Ser Ile Ala Ser Lys Val Asn Ser Ile Ala Leu
290 295 300

Gly Ser Asn Ser Leu Ser Ser Gly Glu Asn Ala Ile Ala Leu Gly Glu
305 310 315 320

Gly Ser Ala Ala Gly Gly Ser Asn Ser Leu Ala Phe Gly Ser Gln Ser
325 330 335

Arg Ala Asn Gly Asn Asp Ser Val Ala Ile Gly Val Gly Ala Ala Ala
340 345 350

Ala Thr Asp Asn Ser Val Ala Ile Gly Ala Gly Ser Thr Thr Asp Ala
355 360 365

Ser Asn Thr Val Ser Val Gly Asn Ser Ala Thr Lys Arg Lys Ile Val
370 375 380

Asn Met Ala Ala Gly Ala Ile Ser Asn Thr Ser Thr Asp Ala Ile Asn
385 390 395 400

Gly Ser Gln Leu Tyr Thr Ile Ser Asp Ser Val Ala Lys Arg Leu Gly
405 410 415

Gly Gly Ala Thr Val Gly Ser Asp Gly Thr Val Thr Ala Val Ser Tyr
420 425 430

Ala Leu Arg Ser Gly Thr Tyr Asn Asn Val Gly Asp Ala Leu Ser Gly
435 440 445

Ile Asp Asn Asn Thr Leu Gln Trp Asn Lys Thr Ala Gly Ala Phe Ser
450 455 460

Ala Asn His Gly Ala Asn Ala Thr Asn Lys Ile Thr Asn Val Ala Lys
465 470 475 480

Gly Thr Val Ser Ala Thr Ser Thr Asp Val Val Asn Gly Ser Gln Leu
485 490 495

Tyr Asp Leu Gln Gln Asp Ala Leu Leu Trp Asn Gly Thr Ala Phe Ser

500 505 510

Ala Ala His Gly Thr Glu Ala Thr Ser Lys Ile Thr Asn Val Thr Ala
515 520 525

Gly Asn Leu Thr Ala Gly Ser Thr Asp Ala Val Asn Gly Ser Gln Leu
530 535 540

Lys Thr Thr Asn Asp Asn Val Thr Thr Asn Thr Thr Asn Ile Ala Thr
545 550 555 560

Asn Thr Thr Asn Ile Thr Asn Leu Thr Asp Ala Val Asn Gly Leu Gly
565 570 575

Asp Asp Ser Leu Leu Trp Asn Lys Ala Ala Gly Ala Phe Ser Ala Ala
580 585 590

His Gly Thr Glu Ala Thr Ser Lys Ile Thr Asn Val Thr Ala Gly Asn
595 600 605

Leu Thr Ala Gly Ser Thr Asp Ala Val Asn Gly Ser Gln Leu Lys Thr
610 615 620

Thr Asn Asp Asn Val Thr Thr Asn Thr Thr Asn Ile Ala Thr Asn Thr
625 630 635 640

Thr Asn Ile Thr Asn Leu Thr Asp Ala Val Asn Gly Leu Gly Asp Asp
645 650 655

Ser Leu Leu Trp Asn Lys Thr Ala Gly Ala Phe Ser Ala Ala His Gly
660 665 670

Thr Asp Ala Thr Ser Lys Ile Thr Asn Val Thr Ala Gly Asn Leu Thr
675 680 685

Ala Gly Ser Thr Asp Ala Val Asn Gly Ser Gln Leu Lys Thr Thr Asn
690 695 700

Asp Asn Val Thr Thr Asn Thr Thr Asn Ile Ala Thr Asn Thr Thr Asn
705 710 715 720

Ile Thr Asn Leu Thr Asp Ala Val Asn Gly Leu Gly Asp Asp Ser Leu
725 730 735

Leu Trp Asn Lys Thr Ala Gly Ala Phe Ser Ala Ala His Gly Thr Asp
740 745 750

Ala Thr Ser Lys Ile Thr Asn Val Lys Ala Gly Asp Leu Thr Ala Gly
755 760 765

Ser Thr Asp Ala Val Asn Gly Ser Gln Leu Lys Thr Thr Asn Asp Asn
770 775 780

Val Ser Thr Asn Thr Thr Asn Ile Thr Asn Leu Thr Asp Ala Val Asn
785 790 795 800

Gly Leu Gly Asp Asp Ser Leu Leu Trp Asn Lys Thr Ala Gly Ala Phe
805 810 815

Ser Ala Ala His Gly Thr Asp Ala Thr Ser Lys Ile Thr Asn Val Lys
820 825 830

Ala Gly Asp Leu Thr Ala Gly Ser Thr Asp Ala Val Asn Gly Ser Gln
835 840 845

Leu Lys Thr Thr Asn Asp Asn Val Ser Thr Asn Thr Thr Asn Ile Thr
850 855 860

Asn Leu Thr Asp Ser Val Gly Asp Leu Lys Asp Asp Ser Leu Leu Trp
865 870 875 880

Asn Lys Ala Ala Gly Ala Phe Ser Ala Ala His Gly Thr Glu Ala Thr
885 890 895

Ser Lys Ile Thr Asn Leu Leu Ala Gly Lys Ile Ser Ser Asn Ser Thr
900 905 910

Asp Ala Ile Asn Gly Ser Gln Leu Tyr Gly Val Ala Asp Ser Phe Thr
915 920 925

Ser Tyr Leu Gly Gly Gly Ala Asp Ile Ser Asp Thr Gly Val Leu Ser
930 935 940

Gly Pro Thr Tyr Thr Ile Gly Gly Thr Asp Tyr Thr Asn Val Gly Asp
945 950 955 960

Ala Leu Ala Ala Ile Asn Thr Ser Phe Ser Thr Ser Leu Gly Asp Ala
965 970 975

Leu Leu Trp Asp Ala Thr Ala Gly Lys Phe Ser Ala Lys His Gly Ile
980 985 990

Asn Asn Ala Pro Ser Val Ile Thr Asp Val Ala Asn Gly Ala Val Ser
995 1000 1005

Ser Thr Ser Ser Asp Ala Ile Asn Gly Ser Gln Leu Tyr Gly Val
1010 1015 1020

Ser Asp Tyr Ile Ala Asp Ala Leu Gly Gly Asn Ala Val Val Asn
1025 1030 1035

Thr Asp Gly Ser Ile Thr Thr Pro Thr Tyr Ala Ile Ala Gly Gly
1040 1045 1050

Ser Tyr Asn Asn Val Gly Asp Ala Leu Glu Ala Ile Asp Thr Thr
1055 1060 1065

Leu Asp Asp Ala Leu Leu Trp Asp Thr Thr Ala Asn Gly Gly Asn
1070 1075 1080

Gly Ala Phe Ser Ala Ala His Gly Lys Asp Lys Thr Ala Ser Val
1085 1090 1095

Ile Thr Asn Val Ala Asn Gly Ala Val Ser Ala Thr Ser Asn Asp
1100 1105 1110

Ala Ile Asn Gly Ser Gln Leu Tyr Ser Thr Asn Lys Tyr Ile Ala
1115 1120 1125

Asp Ala Leu Gly Gly Asp Ala Glu Val Asn Ala Asp Gly Thr Ile
1130 1135 1140

Thr Ala Pro Thr Tyr Thr Ile Ala Asn Thr Asp Tyr Asn Asn Val
1145 1150 1155

Gly Glu Ala Leu Asp Ala Leu Asp Asn Asn Ala Leu Leu Trp Asp
1160 1165 1170

Glu Asp Ala Gly Ala Tyr Asn Ala Ser His Asp Gly Asn Ala Ser
1175 1180 1185

Lys Ile Thr Asn Val Ala Ala Gly Asp Leu Ser Thr Thr Ser Thr
1190 1195 1200

Asp Ala Val Asn Gly Ser Gln Leu Asn Ala Thr Asn Ile Leu Val
1205 1210 1215

Thr Gln Asn Ser Gln Met Ile Asn Gln Leu Ala Gly Asn Thr Ser
1220 1225 1230

Glu Thr Tyr Ile Glu Glu Asn Gly Ala Gly Ile Asn Tyr Val Arg
1235 1240 1245

Thr Asn Asp Ser Gly Leu Ala Phe Asn Asp Ala Ser Ala Ser Gly
1250 1255 1260

Ile Gly Ala Thr Ala Val Gly Tyr Asn Ala Val Ala Ser His Ala
1265 1270 1275

Ser Ser Val Ala Ile Gly Gln Asp Ser Ile Ser Glu Val Asp Thr
1280 1285 1290

Gly Ile Ala Leu Gly Ser Ser Ser Val Ser Ser Arg Val Ile Val
1295 1300 1305

Lys Gly Thr Arg Asn Thr Ser Val Ser Glu Glu Gly Val Val Ile
1310 1315 1320

Gly Tyr Asp Thr Thr Asp Gly Glu Leu Leu Gly Ala Leu Ser Ile
1325 1330 1335

Gly Asp Asp Gly Lys Tyr Arg Gln Ile Ile Asn Val Ala Asp Gly
1340 1345 1350

Ser Glu Ala His Asp Ala Val Thr Val Arg Gln Leu Gln Asn Ala
1355 1360 1365

Ile Gly Ala Val Ala Thr Thr Pro Thr Lys Tyr Tyr His Ala Asn
1370 1375 1380

Ser Thr Ala Glu Asp Ser Leu Ala Val Gly Glu Asp Ser Leu Ala

1385 1390 1395

Met Gly Ala Lys Thr Ile Val Asn Gly Asn Ala Gly Ile Gly Ile
1400 1405 1410

Gly Leu Asn Thr Leu Val Leu Ala Asp Ala Ile Asn Gly Ile Ala
1415 1420 1425

Ile Gly Ser Asn Ala Arg Ala Asn His Ala Asp Ser Ile Ala Met
1430 1435 1440

Gly Asn Gly Ser Gln Thr Thr Arg Gly Ala Gln Thr Asn Tyr Thr
1445 1450 1455

Ala Tyr Asn Met Asp Ala Pro Gln Asn Ser Val Gly Glu Phe Ser
1460 1465 1470

Val Gly Ser Glu Asp Gly Gln Arg Gln Ile Thr Asn Val Ala Ala
1475 1480 1485

Gly Ser Ala Asp Thr Asp Ala Val Asn Val Gly Gln Leu Lys Val
1490 1495 1500

Thr Asp Ala Gln Val Ser Gln Asn Thr Gln Ser Ile Thr Asn Leu
1505 1510 1515

Asn Thr Gln Val Thr Asn Leu Asp Thr Arg Val Thr Asn Ile Glu
1520 1525 1530

Asn Gly Ile Gly Asp Ile Val Thr Thr Gly Ser Thr Lys Tyr Phe
1535 1540 1545

Lys Thr Asn Thr Asp Gly Ala Asp Ala Asn Ala Gln Gly Lys Asp
1550 1555 1560

Ser Val Ala Ile Gly Ser Gly Ser Ile Ala Ala Ala Asp Asn Ser
1565 1570 1575

Val Ala Leu Gly Thr Gly Ser Val Ala Asp Glu Glu Asn Thr Ile
1580 1585 1590

Ser Val Gly Ser Ser Thr Asn Gln Arg Arg Ile Thr Asn Val Ala
1595 1600 1605

Ala Gly Val Asn Ala Thr Asp Ala Val Asn Val Ser Gln Leu Lys
1610 1615 1620

Ser Ser Glu Ala Gly Gly Val Arg Tyr Asp Thr Lys Ala Asp Gly
1625 1630 1635

Ser Ile Asp Tyr Ser Asn Ile Thr Leu Gly Gly Gly Asn Ser Gly
1640 1645 1650

Thr Thr Arg Ile Ser Asn Val Ser Ala Gly Val Asn Asn Asn Asp
1655 1660 1665

Ala Val Asn Tyr Ala Gln Leu Lys Gln Ser Val Gln Glu Thr Lys
1670 1675 1680

Gln Tyr Thr Asp Gln Arg Met Val Glu Met Asp Asn Lys Leu Ser
1685 1690 1695

Lys Thr Glu Ser Lys Leu Ser Gly Gly Ile Ala Ser Ala Met Ala
1700 1705 1710

Met Thr Gly Leu Pro Gln Ala Tyr Thr Pro Gly Ala Ser Met Ala
1715 1720 1725

Ser Ile Gly Gly Gly Thr Tyr Asn Gly Glu Ser Ala Val Ala Leu
1730 1735 1740

Gly Val Ser Met Val Ser Ala Asn Gly Arg Trp Val Tyr Lys Leu
1745 1750 1755

Gln Gly Ser Thr Asn Ser Gln Gly Glu Tyr Ser Ala Ala Leu Gly
1760 1765 1770

Ala Gly Ile Gln Trp
1775

<210> 35
<211> 227
<212> PRT
<213> Escherichia coli
<400> 35

Met Asn Leu Lys Lys Thr Leu Leu Ser Val Leu Met Ile Leu Gln Leu

1 5 10 15

Cys Leu Leu Val Gly Cys Asp Tyr Ile Glu Lys Ala Ser Lys Val Asp
20 25 30

Asp Leu Val Thr Gln Gln Glu Leu Gln Lys Ser Lys Ile Glu Ala Leu
35 40 45

Glu Lys Gln Gln Glu Leu Asp Lys Arg Lys Ile Glu His Phe Glu Lys
50 55 60

Gln Gln Thr Thr Ile Ile Asn Ser Thr Lys Thr Leu Ala Gly Val Val
65 70 75 80

Lys Ala Val Lys Asn Lys Gln Asp Glu Phe Val Phe Thr Glu Phe Asn
85 90 95

Pro Ala Gln Thr Gln Tyr Phe Ile Leu Asn Asn Gly Ser Val Gly Leu
100 105 110

Ala Gly Lys Ile Leu Ser Ile Asp Ala Val Glu Asn Gly Ser Val Ile
115 120 125

Arg Ile Ser Leu Val Asn Leu Leu Ser Val Pro Val Ser Asn Met Gly
130 135 140

Phe Tyr Ala Thr Trp Gly Gly Glu Lys Pro Thr Asp Ile Asn Ala Leu
145 150 155 160

Ala Lys Trp Gln Gln Leu Leu Phe Ser Thr Ala Met Asn Ser Ser Leu
165 170 175

Lys Leu Leu Pro Gly Gln Trp Gln Asp Ile Asn Leu Thr Leu Lys Gly
180 185 190

Val Ser Pro Asn Asn Leu Lys Tyr Leu Lys Leu Ala Ile Asn Met Ala
195 200 205

Asn Ile Gln Phe Asp Arg Leu Gln Pro Ala Glu Ser Pro Gln Arg Lys
210 215 220

Asn Lys Lys
225

<210> 36
<211> 1109
<212> PRT
<213> Escherichia coli
<400> 36

Met Lys Arg Val Val Arg Leu Leu Gly Val Gly Leu Leu Leu Leu Val
1 5 10 15

Val Leu Leu Leu Ile Leu Phe Val Leu Ala Gln Thr Thr Pro Leu Ile
20 25 30

Ser Ala Gln Asp Glu His Ala Val Trp Leu Arg Leu Leu Ile Thr Ala
35 40 45

Ile Val Ile Cys Leu Leu Ser Met Cys Ile Phe Phe Leu Phe Ser Phe
50 55 60

Arg Gln Asn Glu Ala Ser Thr Ile Ser Leu Tyr Ala Gln Pro Thr Asp
65 70 75 80

Ile Lys Glu Ile Asn Thr Glu Gln Pro Asn Tyr Ala Ser Leu Leu Thr
85 90 95

Ile Tyr Leu Arg Asp Arg Tyr Gly Pro Phe Trp Arg Arg Lys Val Arg
100 105 110

Leu Leu Leu Val Thr Gly Glu Pro Glu Gln Ala Glu Ala Ile Ala Pro
115 120 125

Gly Leu Thr Gly Gln His Trp Leu Glu Gly Asp His Thr Val Leu Ile
130 135 140

Tyr Gly Gly Arg Pro Thr Ala Glu Pro Asp Val Thr Leu Leu Thr Ala
145 150 155 160

Leu Lys Lys Leu Arg Arg Ser Arg Pro Leu Asp Gly Ile Ile Trp Ala
165 170 175

Leu Thr Glu Glu Gln Ser Arg Gln Thr Ala Gln Leu Asp Lys Gly Trp
180 185 190

Arg Gly Leu Ile Asn Gly Gly Lys Arg Leu Gly Phe Gln Ala Pro Leu

195 200 205

Tyr Leu Trp Gln Val Cys Asp Asp Gly Asp Tyr Gln Thr Gly Arg Pro
210 215 220

Leu Gln Ser Val Gly Cys Leu Leu Pro Glu Arg Cys Thr Pro Glu Gln
225 230 235 240

Leu Ala Val Met Leu Glu Ala Ala Ala Asp Gly Thr Gly His Val Ala
245 250 255

Ala Thr Asp Arg Tyr Arg Met Phe Ser Ala Ala Ser Gly Ser Tyr Pro
260 265 270

Cys Arg Ala Gly Tyr Cys Ser Leu Ala Asp Arg Pro Glu Thr Ala Ala
275 280 285

Gly Arg Arg Arg Ile Phe Phe Pro Ala Pro Ala Arg Pro Asp Val Gln
290 295 300

Pro Ala Ala Cys Arg Arg Ala Gly Gly Gln His Leu Met Gln Trp Leu
305 310 315 320

Pro Ser Pro Val Trp Ala Gly Val Thr Val Ile Thr Arg Ala Gly Ala
325 330 335

Arg Trp Val Phe Leu Trp Leu Arg Thr Ala Leu Met Ser Ala Val Cys
340 345 350

Val Leu Val Ile Trp Gly Ala Gly Met Thr Thr Ser Phe Phe Ala Asn
355 360 365

Arg Ala Leu Val Gln Glu Thr Gly Ile Gln Thr Ala Arg Ala Leu Asp
370 375 380

Thr Arg Leu Pro Leu Ala Glu Gln Leu Val Ala Leu His Thr Leu Gln
385 390 395 400

Gly Glu Leu Glu Arg Leu Gln Tyr Arg Ile Arg Glu Gly Ala Pro Trp
405 410 415

Tyr Gln Arg Phe Gly Leu Glu Arg Asn Gln Gln Leu Leu Ala Ala Ala
420 425 430

Phe Pro Gly Tyr Ala Gln Ala Ala Asn Arg Leu Val Arg Asp Val Ala
435 440 445

Val Asp His Leu Gln Gln Gln Leu Asn Ala Phe Val Ala Leu Pro Pro
450 455 460

Asn Ser Pro Gln Arg Thr Ala Thr Gly Glu Gln Arg Tyr Lys Gln Leu
465 470 475 480

Lys Ala Leu Leu Met Thr Ser Arg Pro Glu Lys Ala Asp Ala Ala Phe
485 490 495

Phe Ser Thr Thr Leu Met Ala Asp Gly Leu Arg Tyr Glu Asn Ile Pro
500 505 510

Glu Gly Val Arg Gln Ser Val Leu Pro Ser Leu Leu Thr Phe Trp Thr
515 520 525

Ala Asn Leu Pro Glu His Pro Gln Trp Lys Thr Ser Pro Pro Pro Glu
530 535 540

Leu Thr Gly Ala Val Arg Lys Ile Leu Leu Arg Gln Ile Gly Val Arg
545 550 555 560

Asn Ala Glu Asn Thr Leu Tyr Gln Asn Val Leu Gln Gln Val Ser Arg
565 570 575

Asn Tyr Ala Asp Met Thr Leu Ala Asp Met Thr Gly Asp Thr Leu Thr
580 585 590

Glu Ser Leu Phe Ser Thr Glu Gln Thr Val Pro Gly Met Phe Thr Arg
595 600 605

Gln Ala Trp Glu Gly Gln Val Arg Glu Ala Ile Glu Gln Val Val Thr
610 615 620

Ala Arg Arg Glu Glu Ile Asp Trp Val Leu Ser Asp Arg Gln Gln Asp
625 630 635 640

Thr Ser Ala Asp Ile Ser Pro Asp Thr Leu Arg Asn Arg Leu Thr Ser
645 650 655

Arg Tyr Phe Thr Asp Phe Ala Gly Ser Trp Leu Ala Phe Leu Asn Ser
660 665 670

Ile His Trp Lys Lys Glu Asp Ser Leu Ser Gly Ile Leu Asp Gln Leu
675 680 685

Thr Leu Met Ala Asp Ala Arg Gln Ser Pro Leu Ile Ala Leu Thr Asp
690 695 700

Thr Leu Ala Trp Gln Ala Ala Thr Gly Arg Glu Asn Arg Gly Leu Ser
705 710 715 720

Asp Ser Leu Ala Lys Ser Ala Gln Glu Leu Phe Asn Gly Lys Glu Lys
725 730 735

Thr Pro Gln Gln Ser Arg Glu Gly Asp Asp Val Pro Val Gly Pro Leu
740 745 750

Asp Lys Thr Phe Thr Pro Leu Leu Arg Leu Leu Gly Asp Lys Ala Gly
755 760 765

Gly Gly Asp Ser Gln Leu Ser Leu Gln Thr Tyr Leu Thr Arg Val Thr
770 775 780

Arg Val Arg Leu Lys Leu Gln Gln Val Thr Asn Ala Pro Asp Pro Gln
785 790 795 800

Glu Met Thr Gln Gln Leu Ala Gln Thr Val Leu Gln Gly Lys Thr Val
805 810 815

Asp Leu Thr Asp Thr Arg Asp Tyr Gly Arg Leu Ile Ala Ala Ser Leu
820 825 830

Gly Glu Glu Trp Ser Gly Phe Gly Gln Ala Leu Phe Val Arg Pro Val
835 840 845

Glu Gln Ser Trp Arg Gln Val Leu Thr Pro Ala Ala Asp Ser Leu Asn
850 855 860

Arg Gln Trp Gln Arg Ala Ile Val Ser His Trp Asn Gln Asp Phe Ala
865 870 875 880

Gly Arg Tyr Pro Phe Lys Ala Ser Gln Asn Asp Ala Ser Leu Pro Leu
885 890 895

Leu Ala Gln Tyr Leu Arg Asp Asp Gly Arg Ile Asn Leu Phe Ile Ala
900 905 910

Ala Asn Leu Ser Gly Val Leu Lys Arg Glu Gly Arg Tyr Trp Val Ala
915 920 925

Asp Ala Met Asn Thr Gln Gly Leu Thr Val Asn Pro Asp Phe Ile Arg
930 935 940

Ala Leu Asn Arg Leu Arg Asp Val Ala Asp Thr Ala Phe Ala Ser Gly
945 950 955 960

Asp Ala Gly Ile His Phe Glu Leu Arg Ala Lys Pro Ala Arg Asp Val
965 970 975

Met Lys Thr His Leu Val Ile Asp Gly Gln Glu Leu Glu Tyr Phe Asn
980 985 990

Gln Lys Glu Arg Trp Gln Arg Phe Asn Trp Pro Asp Glu Gln Trp Gln
995 1000 1005

Pro Gly Ala Ser Leu Ser Trp Thr Ser Thr Gln Ala Met Glu Arg
1010 1015 1020

Ile Leu Ala Asp Tyr Arg Gly Ser Trp Ser Leu Ile Arg Leu Leu
1025 1030 1035

Glu Gln Ala Gln Val Thr Pro Val Asp Ser Ser Thr Phe Lys Val
1040 1045 1050

Val Trp Lys Ala Gln Asp Gly Leu Pro Leu Asn Tyr Leu Leu Arg
1055 1060 1065

Val Glu Gln Gly Lys Gly Pro Leu Ala Leu Leu Glu Leu Lys Asn
1070 1075 1080

Phe Arg Leu Pro Gly Gln Val Phe Leu Thr Gly Lys Ser Met Lys
1085 1090 1095

Asp Val Glu Glu Tyr Gly Glu Asp Ala Asp Glu

1100 1105

<210> 37
<211> 178
<212> PRT
<213> Escherichia coli
<400> 37

Met Phe Pro Ile Arg Phe Lys Arg Pro Ala Leu Leu Cys Met Ala Met
1 5 10 15

Leu Thr Val Val Leu Ser Gly Cys Gly Leu Ile Gln Lys Val Val Asp
20 25 30

Glu Ser Lys Ser Val Ala Ser Ala Val Phe Tyr Lys Gln Ile Lys Ile
35 40 45

Leu His Leu Asp Phe Phe Ser Arg Ser Ala Leu Asn Thr Asp Ala Glu
50 55 60

Asp Thr Pro Leu Ser Thr Met Val His Val Trp Gln Leu Lys Thr Arg
65 70 75 80

Glu Asp Phe Asp Lys Ala Asp Tyr Asp Thr Leu Phe Met Gln Glu Glu
85 90 95

Lys Thr Leu Glu Lys Asp Val Leu Ala Lys His Thr Val Trp Val Lys
100 105 110

Pro Glu Gly Thr Ala Ser Leu Asn Val Pro Leu Asp Lys Glu Thr Gln
115 120 125

Phe Val Ala Ile Ile Gly Gln Phe Tyr His Pro Asp Glu Lys Ser Asp
130 135 140

Ser Trp Arg Leu Val Ile Lys Arg Asp Glu Leu Glu Ala Asp Lys Pro
145 150 155 160

Arg Ser Ile Glu Leu Met Arg Ser Asp Leu Arg Leu Leu Pro Leu Lys
165 170 175

Asp Lys

<210> 38
<211> 280
<212> PRT
<213> Escherichia coli
<400> 38

Met Ile Ser Gly Gly Asn Met Leu Lys Glu Trp Met Ile Phe Thr Cys
1 5 10 15

Ser Leu Leu Thr Leu Ala Gly Ala Ser Leu Pro Leu Ser Gly Cys Ile
20 25 30

Ser Arg Gly Gln Glu Ser Ile Ser Glu Gly Ala Ala Phe Gly Ala Gly
35 40 45

Ile Leu Arg Glu Pro Gly Ala Thr Lys Lys Ala Asp Thr Lys Asp Leu
50 55 60

Asn Val Pro Pro Pro Val Tyr Gly Pro Pro Gln Val Ile Phe Arg Ile
65 70 75 80

Asp Asp Asn Arg Tyr Phe Thr Leu Glu Asn Tyr Thr His Cys Glu Asn
85 90 95

Gly Gln Thr Phe Tyr Asn Asn Lys Ala Lys Asn Ile His Val Lys Ile
100 105 110

Leu Asp Ala Ser Gly Tyr Leu Phe Lys Gly Arg Leu Phe Trp Leu Ser
115 120 125

Thr Arg Asp Asp Phe Leu Ala Phe Pro Ala Thr Leu Asn Thr Arg His
130 135 140

Ala Ser Cys Met Gly Ser Asn Lys Gly Cys Met Asn Ala Val Ile Val
145 150 155 160

Thr Thr Asp Gly Gly Lys Arg Arg Ser Gly Val Pro Tyr Gly Ser Tyr
165 170 175

Thr Gln Asn Pro Thr Gly Ala Thr Arg Asp Tyr Asp Met Leu Val Met
180 185 190

Asn Asp Gly Phe Tyr Leu Leu Arg Tyr Arg Gly Gly Gln Gly Arg Phe
195 200 205

Ser Pro Val Ile Leu Arg Trp Ile Leu Ser Thr Glu Asp Ser Ser Gly
210 215 220

Val Val Arg Ser Glu Asp Ala Tyr Glu Leu Phe Arg Pro Gly Glu Glu
225 230 235 240

Val Pro Ser Thr Gly Phe Tyr Lys Ile Asp Leu Ser Arg Phe Tyr Pro
245 250 255

Lys Asn Asn Val Met Glu Met Gln Cys Asp Arg Thr Leu Glu Pro Val
260 265 270

Gln Pro Ser Glu Ser Lys Ile Gln
275 280

<210> 39
<211> 501
<212> PRT
<213> Escherichia coli
<400> 39

Met Glu His Val Ser Ile Lys Thr Leu Tyr His Leu Leu Cys Cys Met
1 5 10 15

Leu Leu Phe Ile Ser Ala Met Cys Ala Leu Ala Gln Glu His Glu Pro
20 25 30

Ile Gly Ala Gln Asp Glu Arg Leu Ser Thr Leu Ile His Gln Arg Met
35 40 45

Gln Glu Ala Lys Val Pro Ala Leu Ser Val Ser Val Thr Ile Lys Gly
50 55 60

Val Arg Gln Arg Phe Val Tyr Gly Val Ala Asp Val Ala Ser Gln Lys
65 70 75 80

Ala Asn Thr Leu Asp Thr Val Tyr Glu Leu Gly Ser Met Ser Lys Ala
85 90 95

Phe Thr Gly Leu Val Val Gln Ile Leu Ile Gln Glu Gly Arg Leu Arg
100 105 110

Gln Gly Asp Asp Ile Ile Thr Tyr Leu Pro Glu Met Arg Leu Asn Tyr
115 120 125

```
Gln Gly Lys Pro Ala Ser Leu Thr Val Ala Asp Phe Leu Tyr His Thr
    130                 135                 140

Ser Gly Leu Pro Phe Ser Thr Leu Ala Arg Leu Glu Asn Pro Met Pro
145                 150                 155                 160

Gly Ser Ala Val Ala Gln Gln Leu Arg Asn Glu Asn Leu Leu Phe Ala
                165                 170                 175

Pro Gly Ala Lys Phe Ser Tyr Ala Ser Ala Asn Tyr Asp Val Leu Gly
            180                 185                 190

Ala Val Ile Glu Asn Val Thr Gly Lys Thr Phe Thr Glu Val Ile Ala
        195                 200                 205

Glu Arg Leu Thr Gln Pro Leu Gly Met Ser Ala Thr Val Ala Val Lys
    210                 215                 220

Gly Asp Glu Ile Ile Val Asn Lys Ala Ser Gly Tyr Lys Leu Gly Phe
225                 230                 235                 240

Gly Lys Pro Val Leu Phe His Ala Pro Leu Ala Arg Asn His Val Pro
                245                 250                 255

Ala Ala Tyr Ile His Ser Thr Leu Pro Asp Met Glu Ile Trp Ile Asp
            260                 265                 270

Ala Trp Leu His Arg Lys Ala Leu Pro Ala Thr Leu Arg Glu Ala Met
        275                 280                 285

Ser Asn Ser Trp Arg Gly Asn Ser Asp Val Pro Leu Ala Ala Asp Asn
    290                 295                 300

Arg Ile Leu Tyr Ala Ser Gly Trp Phe Ile Asp Gln Asn Gln Gly Pro
305                 310                 315                 320

Tyr Ile Ser His Gly Gly Gln Asn Pro Asn Phe Ser Ser Cys Ile Ala
                325                 330                 335

Leu Arg Pro Asp Gln Gln Ile Gly Ile Val Ala Leu Ala Asn Met Asn
            340                 345                 350
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Ser Asn Leu Ile Leu Gln Leu Cys Ala Asp Ile Asp Asn Tyr Leu Arg
355 360 365

Ile Gly Lys Tyr Ala Asp Gly Ala Gly Asp Ala Ile Thr Ala Thr Asp
370 375 380

Thr Leu Phe Val Tyr Leu Thr Leu Leu Leu Cys Phe Trp Gly Ala Val
385 390 395 400

Val Val Val Arg Gly Ala Phe Arg Val Tyr Arg Ala Thr Ala His Gly
405 410 415

Pro Gly Lys Gln Gln Arg Leu Arg Leu Arg Val Arg Asp Tyr Ile Ile
420 425 430

Ala Leu Ala Val Pro Gly Leu Val Ala Ala Met Leu Tyr Val Ala Pro
435 440 445

Gly Ile Leu Ser Pro Gly Leu Asp Trp Arg Phe Ile Leu Val Trp Gly
450 455 460

Pro Ser Ser Val Leu Ala Ile Pro Phe Gly Ile Ile Leu Leu Ala Phe
465 470 475 480

Val Leu Thr Leu Asn His Gln Ile Lys Arg Ile Leu Leu His Asn Lys
485 490 495

Glu Trp Asp Asp Glu
500

<210> 40
<211> 682
<212> PRT
<213> Escherichia coli
<400> 40

Met Lys Asn Lys Tyr Ile Ile Ala Pro Gly Ile Ala Val Met Cys Ser
1 5 10 15

Ala Val Ile Ser Ser Gly Tyr Ala Ser Ser Asp Lys Lys Glu Asp Thr
20 25 30

Leu Val Val Thr Ala Ser Gly Phe Thr Gln Gln Leu Arg Asn Ala Pro
35 40 45

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Ala Ser Val Ser Val Ile Thr Ser Glu Gln Leu Gln Lys Lys Pro Val
    50                  55                  60

Ser Asp Leu Val Asp Ala Val Lys Asp Val Glu Gly Ile Ser Ile Thr
65                  70                  75                  80

Gly Gly Asn Glu Lys Pro Asp Ile Ser Ile Arg Gly Leu Ser Gly Asp
                85                  90                  95

Tyr Thr Leu Ile Leu Val Asp Gly Arg Arg Gln Ser Gly Arg Glu Ser
            100                 105                 110

Arg Pro Asn Gly Ser Gly Gly Phe Glu Ala Gly Phe Ile Pro Pro Val
        115                 120                 125

Glu Ala Ile Glu Arg Ile Glu Val Ile Arg Gly Pro Met Ser Ser Leu
    130                 135                 140

Tyr Gly Ser Asp Ala Ile Gly Gly Val Ile Asn Ile Ile Thr Lys Pro
145                 150                 155                 160

Val Asn Asn Gln Thr Trp Asp Gly Val Leu Gly Leu Gly Gly Ile Ile
                165                 170                 175

Gln Glu His Gly Lys Phe Gly Asn Ser Thr Thr Asn Asp Phe Tyr Leu
            180                 185                 190

Ser Gly Pro Leu Ile Lys Asp Lys Leu Gly Leu Gln Leu Tyr Gly Gly
        195                 200                 205

Met Asn Tyr Arg Lys Glu Asp Ser Ile Ser Gln Gly Thr Pro Ala Lys
    210                 215                 220

Asp Asn Lys Asn Ile Thr Ala Thr Leu Gln Phe Thr Pro Thr Glu Ser
225                 230                 235                 240

Gln Lys Phe Val Phe Glu Tyr Gly Lys Asn Asn Gln Val His Thr Leu
                245                 250                 255

Thr Pro Gly Glu Ser Leu Asp Ala Trp Thr Met Arg Gly Asn Leu Lys
            260                 265                 270
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Gln Pro Asn Ser Lys Arg Glu Thr His Asn Ser Arg Ser His Trp Val
        275                 280                 285

Ala Ala Trp Asn Ala Gln Gly Glu Ile Leu His Pro Glu Ile Ala Val
    290                 295                 300

Tyr Gln Glu Lys Val Ile Arg Glu Val Lys Ser Gly Lys Lys Asp Lys
305                 310                 315                 320

Tyr Asn His Trp Asp Leu Asn Tyr Glu Ser Arg Lys Pro Glu Ile Thr
                325                 330                 335

Asn Thr Ile Ile Asp Ala Lys Val Thr Ala Phe Leu Pro Glu Asn Val
            340                 345                 350

Leu Thr Ile Gly Gly Gln Phe Gln His Ala Glu Leu Arg Asp Asp Ser
        355                 360                 365

Ala Thr Gly Lys Lys Thr Thr Glu Thr Gln Ser Val Ser Ile Lys Gln
    370                 375                 380

Lys Ala Val Phe Ile Glu Asn Glu Tyr Ala Ala Thr Asp Ser Leu Ala
385                 390                 395                 400

Leu Thr Gly Gly Leu Arg Leu Asp Asn His Glu Ile Tyr Gly Ser Tyr
                405                 410                 415

Trp Asn Pro Arg Leu Tyr Ala Val Tyr Asn Leu Thr Asp Asn Leu Thr
            420                 425                 430

Leu Lys Gly Gly Ile Ala Lys Ala Phe Arg Ala Pro Ser Ile Arg Glu
        435                 440                 445

Val Ser Pro Gly Phe Gly Thr Leu Thr Gln Gly Gly Ala Ser Ile Met
    450                 455                 460

Tyr Gly Asn Arg Asp Leu Lys Pro Glu Thr Ser Val Thr Glu Glu Ile
465                 470                 475                 480

Gly Ile Ile Tyr Ser Asn Asp Ser Gly Phe Ser Ala Ser Ala Thr Leu
                485                 490                 495
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Phe Asn Thr Asp Phe Lys Asn Lys Leu Thr Ser Tyr Asp Ile Gly Thr
            500                 505                 510

Lys Asp Pro Val Thr Gly Leu Asn Thr Phe Ile Tyr Asp Asn Val Gly
        515                 520                 525

Glu Ala Asn Ile Arg Gly Val Glu Leu Ala Thr Gln Ile Pro Val Tyr
    530                 535                 540

Asp Lys Trp His Val Ser Ala Asn Tyr Thr Phe Thr Asp Ser Arg Arg
545                 550                 555                 560

Lys Ser Asp Asp Glu Ser Leu Asn Gly Lys Ser Leu Lys Gly Glu Pro
                565                 570                 575

Leu Glu Arg Thr Pro Arg His Ala Ala Asn Ala Lys Leu Glu Trp Asp
            580                 585                 590

Tyr Thr Gln Asp Ile Thr Phe Tyr Ser Ser Leu Asn Tyr Thr Gly Lys
        595                 600                 605

Gln Ile Trp Ala Ala Gln Arg Asn Gly Ala Lys Val Pro Arg Val Arg
    610                 615                 620

Asn Gly Phe Thr Ser Met Asp Ile Gly Leu Asn Tyr Gln Ile Leu Pro
625                 630                 635                 640

Asp Thr Leu Ile Asn Phe Ala Val Leu Asn Val Thr Asp Arg Lys Ser
                645                 650                 655

Glu Asp Ile Asp Thr Ile Asp Gly Asn Trp Gln Val Asp Glu Gly Arg
            660                 665                 670

Arg Tyr Trp Ala Asn Val Arg Val Ser Phe
        675                 680


<210>  41
<211>  164
<212>  PRT
<213>  Escherichia coli
<400>  41

Met Gly Phe Arg Lys Thr Ile Ile Thr Ser Val Gly Leu Ile Phe Ile
1               5                   10                  15
```

Ser Phe Ser Phe Val Ala Lys Cys Ser Gln Leu Lys Asn Leu Asn Asn
20 25 30

Tyr Ser Val Met Leu Cys Gly Lys Val Ser Asn Asn Ile Leu Asp Asp
35 40 45

Ile Gly Gly Tyr Lys Glu Arg Asn Ile Leu Met Leu Arg Ala Ile Lys
50 55 60

Lys Ile Ile Ile Met Thr Ile Val Asn Ile Ile Phe Phe Tyr Ser Phe
65 70 75 80

Gln Ser Thr Ala Asp Glu Met Val Leu Ile Lys Lys Tyr Gly Phe Gly
85 90 95

Leu Glu Arg Asp Ile Lys Gly Arg Pro Leu Ile Tyr Pro Ile Glu Asn
100 105 110

Tyr Asp Glu Cys Lys Lys Lys Cys Asn His Met Asn Tyr Ile Ala Asp
115 120 125

Val Asn Ala Gln Leu Ala Met Ser Lys Lys Asn Asn Arg Ile Phe Ala
130 135 140

Asn Ile Thr Phe Thr Asn Asn Ser Ser Thr Thr Tyr Phe Phe Leu Asn
145 150 155 160

Ile Ile Tyr Leu

<210> 42
<211> 218
<212> PRT
<213> Escherichia coli
<400> 42

Met Asn Gln Ile Lys Asp Asn Lys Val Ile Met Lys Ile Lys Asn Leu
1 5 10 15

Ile Ser Val Ile Leu Leu Ser Gly Gly Ile Met Gly Thr Gly Leu Tyr
20 25 30

Ser Ser Asp Asn His Gln Lys Ile Arg Ser Arg Phe Asn Ile Gln Glu
35 40 45

```
Ser Tyr Cys Ala Ile Lys Thr Asn Gly Val Leu Gly Phe Ser Asn Arg
    50                  55                  60

Lys Asp Val Leu Arg Glu Asn Gly Asp Ser Thr Gly Thr Thr Ser Ser
65                  70                  75                  80

Ser Thr Asn Ala Met Met Leu Met Glu Asn Gly Glu Asn Glu Ile Ser
                85                  90                  95

Leu Glu Ile Gly Ala Leu Arg Trp Phe Ser Asp Lys Pro Ala Ser Thr
            100                 105                 110

Glu Glu Arg Gly His Phe Ser Gln Lys Ala Gly Cys Ser Leu Asp Leu
        115                 120                 125

Val Arg Phe Val Lys Gln Glu Glu Thr Ile Leu Ser Ser Ile Lys Val
    130                 135                 140

Thr Ile Asn Gln Gln Gly Ile Pro Glu Ala Gln Pro Asp Ser Met His
145                 150                 155                 160

Pro Val Ile Arg Lys Glu Ile Leu Ala Glu Gln Ala Glu Pro Gly Phe
                165                 170                 175

Ile Asp Pro Asp Tyr Phe Asn Glu Thr Tyr Phe Pro Lys Gly Met Lys
            180                 185                 190

Val Tyr Gln Phe Thr Gln Lys Val Ser Val Ala Gly Leu Pro Asp Gly
        195                 200                 205

Pro Gly Arg Ser Thr Pro Phe Thr Gly Ala
    210                 215
```

<210> 43
<211> 2732
<212> PRT
<213> Escherichia coli
<400> 43

```
Met His Gln Pro Pro Val Arg Phe Thr Tyr Arg Leu Leu Ser Tyr Leu
1               5                   10                  15

Val Ser Ala Ile Ile Ala Gly Gln Pro Leu Leu Pro Ala Val Gly Ala
```

```
            20                  25                  30

Val Ile Thr Pro Gln Asn Gly Ala Gly Met Asp Lys Ala Ala Asn Gly
        35                  40                  45

Val Pro Val Val Asn Ile Ala Thr Pro Asn Gly Ala Gly Ile Ser His
    50                  55                  60

Asn Arg Phe Thr Asp Tyr Asn Val Gly Lys Glu Gly Leu Ile Leu Asn
65                  70                  75                  80

Asn Ala Thr Gly Lys Leu Asn Pro Thr Gln Leu Gly Gly Leu Ile Gln
                85                  90                  95

Asn Asn Pro Asn Leu Lys Ala Gly Gly Glu Ala Lys Gly Ile Ile Asn
            100                 105                 110

Glu Val Thr Gly Gly Lys Arg Ser Leu Leu Gln Gly Tyr Thr Glu Val
        115                 120                 125

Ala Gly Lys Ala Ala Asn Val Met Val Ala Asn Pro Tyr Gly Ile Thr
    130                 135                 140

Cys Asp Gly Cys Gly Phe Ile Asn Thr Pro His Ala Thr Leu Thr Thr
145                 150                 155                 160

Gly Lys Pro Val Met Asn Ala Asp Gly Ser Leu Gln Ala Leu Glu Val
                165                 170                 175

Thr Glu Gly Ser Ile Thr Ile Asn Gly Ala Gly Leu Asp Gly Thr Arg
            180                 185                 190

Ser Asp Ala Val Ser Ile Ile Ala Arg Ala Thr Glu Val Asn Ala Ala
        195                 200                 205

Leu His Ala Lys Asp Leu Thr Val Thr Ala Gly Ala Asn Arg Val Thr
    210                 215                 220

Ala Asp Gly Arg Val Arg Ala Leu Lys Gly Glu Gly Asp Val Pro Lys
225                 230                 235                 240

Val Ala Val Asp Thr Gly Ala Leu Gly Gly Met Tyr Ala Arg Arg Ile
                245                 250                 255
```

```
His Leu Thr Ser Thr Glu Ser Gly Val Gly Val Asn Leu Gly Asn Leu
            260                 265                 270

Tyr Ala Arg Asp Gly Asp Ile Thr Leu Asp Ala Ser Gly Arg Leu Thr
        275                 280                 285

Val Asn Asn Ser Leu Ala Thr Gly Ala Val Thr Ala Lys Gly Gln Gly
    290                 295                 300

Val Thr Leu Thr Gly Asp His Lys Ala Gly Gly Asn Leu Ser Val Ser
305                 310                 315                 320

Ser Arg Arg Asp Ile Val Leu Ser Asn Gly Thr Leu Asn Ser Asp Lys
                325                 330                 335

Asp Leu Ser Leu Thr Ala Gly Gly Arg Ile Thr Gln Gln Asn Glu Lys
            340                 345                 350

Leu Thr Ala Gly Arg Asp Val Thr Leu Ala Ala Lys Asn Ile Thr Gln
        355                 360                 365

Asp Thr Ala Ser Gln Ile Asn Ala Ala Arg Asp Ile Val Thr Val Ala
    370                 375                 380

Ser Asp Thr Leu Thr Thr Gln Gly Gln Ile Thr Ala Gly Gln Asn Leu
385                 390                 395                 400

Thr Ala Ser Ala Thr Thr Leu Thr Gln Asp Gly Ile Leu Leu Ala Lys
                405                 410                 415

Ser His Ala Gly Leu Asn Ala Gly Thr Leu Asn Asn Ser Gly Ala Val
            420                 425                 430

Gln Gly Ala Thr Leu Thr Leu Gly Ser Thr Thr Leu Ser Asn Ser Gly
        435                 440                 445

Ser Leu Leu Ser Gly Gly Pro Leu Thr Met Asn Thr Arg Asp Phe Thr
    450                 455                 460

Gln Ser Gly Arg Thr Gly Ala Lys Gly Lys Val Asp Ile Met Ala Ser
465                 470                 475                 480
```

```
Gly Lys Leu Thr Ser Thr Gly Leu Leu Val Thr Met His Leu Val Leu
                485                 490                 495

Lys Ala Gln Asp Val Thr Gln Asn Gly Val Leu Ser Gly Gly Lys Gly
            500                 505                 510

Leu Thr Val Ser Ala Thr Ser Ser Gly Lys Lys Ser Val Thr His Ser
        515                 520                 525

Asp Ala Ala Met Thr Leu Asn Val Thr Thr Val Ala Leu Asp Gly Glu
    530                 535                 540

Thr Ser Ala Gly Asp Thr Leu Arg Val Gln Ala Asp Lys Leu Ser Thr
545                 550                 555                 560

Ala Ala Gly Ala Gln Leu Gln Ser Gly Lys Asn Leu Ser Ile Asn Ala
                565                 570                 575

Arg Asp Ala Arg Leu Ala Gly Thr Gln Ala Ala Gln Gln Thr Met Val
            580                 585                 590

Val Asn Ala Ser Glu Lys Leu Thr His Ser Gly Lys Ser Ser Ala Pro
        595                 600                 605

Ser Leu Ser Leu Ser Ala Pro Glu Leu Thr Ser Ser Gly Val Leu Val
    610                 615                 620

Gly Ser Ala Leu Asn Thr Gln Ser Gln Thr Leu Thr Asn Ser Gly Leu
625                 630                 635                 640

Leu Gln Gly Glu Ala Ser Leu Thr Val Asn Thr Gln Arg Leu Asp Asn
                645                 650                 655

Gln Gln Asn Gly Thr Leu Tyr Ser Ala Ala Asp Leu Thr Leu Asp Ile
            660                 665                 670

Pro Asp Ile Arg Asn Ser Gly Leu Ile Thr Gly Asp Asn Gly Leu Met
        675                 680                 685

Leu Asn Ala Val Ser Leu Ser Asn Pro Gly Lys Ile Ile Ala Asp Thr
    690                 695                 700
```

```
Leu Ser Val Arg Ala Thr Thr Leu Asp Gly Asp Gly Leu Leu Gln Gly
705                 710                 715                 720

Ala Gly Ala Leu Ala Leu Ala Gly Asp Thr Leu Ser Gln Gly Ser His
                725                 730                 735

Gly Arg Trp Leu Thr Ala Asp Asp Leu Ser Leu Arg Gly Lys Thr Leu
            740                 745                 750

Asn Thr Ala Gly Thr Thr Gln Gly Gln Asn Ile Thr Val Gln Ala Asp
        755                 760                 765

Arg Trp Ala Asn Ser Gly Ser Val Leu Ala Thr Gly Asn Leu Thr Ala
    770                 775                 780

Ser Ala Thr Gly Gln Leu Thr Ser Thr Gly Asp Ile Met Ser Gln Gly
785                 790                 795                 800

Asp Thr Thr Leu Lys Ala Ala Thr Thr Asp Asn Arg Gly Ser Leu Leu
                805                 810                 815

Ser Ala Gly Thr Leu Ser Leu Asp Gly Asn Ser Leu Asp Asn Arg Gly
            820                 825                 830

Thr Val Gln Gly Asn His Val Thr Ile Arg Gln Asn Ser Val Thr Asn
        835                 840                 845

Ser Gly Thr Leu Thr Gly Ile Ala Ala Leu Thr Leu Ala Ala Arg Met
    850                 855                 860

Ala Ser Pro Gln Pro Ala Leu Met Asn Asn Gly Gly Ser Leu Leu Thr
865                 870                 875                 880

Ser Gly Asp Leu Thr Ile Thr Ala Gly Ser Ile Thr Ser Ser Gly His
                885                 890                 895

Trp Gln Gly Lys Arg Val Leu Ile Thr Ala Asp Ser Leu Ala Asn Ser
            900                 905                 910

Gly Ala Ile Gln Ala Ala Asp Ser Leu Thr Ala Arg Leu Thr Gly Glu
        915                 920                 925

Leu Val Ser Thr Ala Gly Ser Lys Val Thr Ser Asn Gly Glu Met Ala
```

930 935 940

Leu Ser Ala Leu Asn Leu Ser Asn Ser Gly Gln Trp Ile Ala Lys Asn
945 950 955 960

Leu Thr Leu Lys Ala Asn Ser Leu Thr Ser Ala Gly Asp Ile Thr Gly
965 970 975

Val Asp Thr Leu Thr Leu Thr Val Asn Gln Thr Leu Asn Asn Gln Ala
980 985 990

Asn Gly Lys Leu Leu Ser Ala Gly Val Leu Thr Leu Lys Ala Asp Ser
995 1000 1005

Val Thr Asn Asp Gly Gln Leu Gln Gly Asn Val Thr Thr Ile Thr
1010 1015 1020

Ala Gly Gln Leu Thr Asn Gly Gly His Leu Gln Gly Glu Thr Leu
1025 1030 1035

Thr Leu Thr Ala Ser Gly Gly Val Asn Asn Arg Ser Gly Gly Val
1040 1045 1050

Leu Met Ser Arg Asn Ala Leu Asn Val Ser Thr Ala Thr Leu Ser
1055 1060 1065

Asn Gln Ser Thr Ile Gln Gly Gly Gly Gly Val Ser Leu Asn Ala
1070 1075 1080

Thr Asp Arg Leu Gln Asn Asp Gly Lys Ile Leu Ser Gly Ser Asn
1085 1090 1095

Leu Thr Leu Thr Ala Gln Val Leu Ala Asn Thr Gly Ser Gly Leu
1100 1105 1110

Val Gln Ala Ala Thr Leu Leu Leu Asp Val Val Asn Thr Val Asn
1115 1120 1125

Gly Gly Arg Val Leu Ala Thr Gly Ser Asp Val Lys Gly Thr Thr
1130 1135 1140

Leu Asn Asn Thr Gly Thr Leu Gln Gly Ala Thr Leu Val Asn Tyr
1145 1150 1155

His Thr Phe Ser Ser Gly Thr Leu Leu Gly Thr Ser Gly Leu Gly
1160 1165 1170

Val Lys Gly Ser Ser Leu Leu Gln Asn Gly Thr Gly Arg Leu Tyr
1175 1180 1185

Ser Ala Gly Asn Leu Leu Leu Asp Ala Gln Asp Phe Ser Gly Gln
1190 1195 1200

Gly Gln Val Val Ala Thr Gly Asp Val Thr Leu Lys Leu Ile Ala
1205 1210 1215

Ala Leu Thr Asn His Gly Thr Leu Ala Ala Gly Lys Thr Leu Ser
1220 1225 1230

Val Thr Ser Gln Asn Ala Ile Thr Asn Gly Gly Val Met Gln Gly
1235 1240 1245

Asp Ala Met Val Leu Gly Ala Gly Glu Ala Phe Thr Asn Asn Gly
1250 1255 1260

Leu Thr Ala Gly Lys Gly Asn Ser Val Phe Ser Ala Gln Arg Leu
1265 1270 1275

Phe Leu Asn Ala Pro Gly Ser Leu Gln Gly Gly Gly Asp Val Ser
1280 1285 1290

Leu Asn Ser Arg Ser Asp Ile Thr Ile Ser Gly Phe Thr Gly Thr
1295 1300 1305

Ala Gly Ser Leu Thr Met Asn Val Ala Gly Thr Leu Leu Asn Ser
1310 1315 1320

Ala Leu Ile Tyr Ala Gly Asn Asn Leu Lys Leu Phe Thr Asp Arg
1325 1330 1335

Leu His Asn Gln His Gly Asp Ile Leu Ala Gly Asn Ser Leu Trp
1340 1345 1350

Val Gln Lys Asp Ala Ser Gly Gly Ala Asn Thr Glu Ile Ile Asn
1355 1360 1365

```
Asn Ser  Gly Asn Ile Glu Thr  His Gln Gly Asp Ile  Val Val Arg
    1370                  1375                  1380

Thr Gly  His Leu Leu Asn Gln  Arg Glu Gly Phe Ser  Ala Thr Thr
    1385                  1390                  1395

Thr Thr  Arg Thr Asn Pro Ser  Ser Ile Gln Gly Met  Gly Asn Ala
    1400                  1405                  1410

Leu Val  Asp Ile Pro Leu Ser  Leu Leu Pro Asp Gly  Ser Tyr Gly
    1415                  1420                  1425

Tyr Phe  Thr Arg Glu Val Glu  Asn Gln His Gly Thr  Pro Cys Asn
    1430                  1435                  1440

Gly His  Gly Ala Cys Asn Ile  Thr Met Asp Thr Leu  Tyr Tyr Tyr
    1445                  1450                  1455

Ala Pro  Phe Ala Asp Ser Ala  Thr Gln Arg Phe Leu  Ser Ser Gln
    1460                  1465                  1470

Asn Ile  Thr Thr Val Thr Gly  Ala Asp Asn Pro Ala  Gly Arg Ile
    1475                  1480                  1485

Ala Ser  Gly Arg Asn Leu Ser  Ala Glu Ala Glu Arg  Leu Glu Asn
    1490                  1495                  1500

Arg Ala  Ser Phe Ile Leu Ala  Asn Gly Asp Ile Ala  Leu Ser Gly
    1505                  1510                  1515

Arg Glu  Leu Ser Asn Gln Ser  Trp Gln Thr Gly Thr  Glu Asn Glu
    1520                  1525                  1530

Tyr Leu  Val Tyr Arg Tyr Asp  Pro Lys Thr Phe Tyr  Gly Ser Tyr
    1535                  1540                  1545

Ala Thr  Gly Ser Leu Asp Lys  Leu Pro Leu Leu Ser  Pro Glu Phe
    1550                  1555                  1560

Glu Asn  Asn Thr Ile Arg Phe  Ser Leu Asp Gly Arg  Glu Lys Asp
    1565                  1570                  1575
```

Tyr Thr Pro Gly Lys Thr Tyr Tyr Ser Val Ile Gln Ala Gly Gly
1580 1585 1590

Asp Val Lys Thr Arg Phe Thr Ser Ser Ile Asn Asn Gly Thr Thr
1595 1600 1605

Thr Ala His Ala Gly Ser Val Ser Pro Val Val Ser Ala Pro Val
1610 1615 1620

Leu Asn Thr Leu Ser Gln Gln Thr Gly Gly Asp Ser Leu Thr Gln
1625 1630 1635

Thr Ala Leu Gln Gln Tyr Glu Pro Val Val Val Gly Ser Pro Gln
1640 1645 1650

Trp His Asp Glu Leu Ala Gly Ala Leu Lys Asn Ile Ala Gly Gly
1655 1660 1665

Ser Pro Leu Thr Gly Gln Thr Gly Ile Ser Asp Asp Trp Pro Leu
1670 1675 1680

Pro Ser Gly Asn Asn Gly Tyr Leu Val Pro Ser Thr Asp Pro Asp
1685 1690 1695

Ser Pro Tyr Leu Ile Thr Val Asn Pro Lys Leu Asp Gly Leu Gly
1700 1705 1710

Gln Val Asp Ser His Leu Phe Ala Gly Leu Tyr Glu Leu Leu Gly
1715 1720 1725

Ala Lys Pro Gly Gln Ala Pro Arg Glu Thr Ala Pro Ser Tyr Thr
1730 1735 1740

Asp Glu Lys Gln Phe Leu Gly Ser Ser Tyr Phe Leu Asp Arg Leu
1745 1750 1755

Gly Leu Lys Pro Glu Lys Asp Tyr Arg Phe Leu Gly Asp Ala Val
1760 1765 1770

Phe Asp Thr Arg Tyr Val Ser Asn Ala Val Leu Ser Arg Thr Gly
1775 1780 1785

Ser Arg Tyr Leu Asn Gly Leu Gly Ser Asp Thr Glu Gln Met Arg

1790 1795 1800

Tyr Leu Met Asp Asn Ala Ala Arg Gln Gln Lys Gly Leu Gly Leu
1805 1810 1815

Glu Phe Gly Val Ala Leu Thr Ala Glu Gln Ile Ala Gln Leu Asp
1820 1825 1830

Gly Ser Ile Leu Trp Trp Glu Ser Val Thr Ile Asn Gly Gln Thr
1835 1840 1845

Val Met Val Pro Lys Leu Tyr Leu Ser Pro Glu Asp Ile Thr Leu
1850 1855 1860

His Asn Gly Ser Val Ile Ser Gly Asn Asn Val Gln Leu Ala Gly
1865 1870 1875

Gly Asn Ile Thr Asn Ser Gly Gly Ser Ile Asn Ala Gln Asn Asp
1880 1885 1890

Leu Ser Leu Asp Ser Ser Gly Tyr Ile Asp Asn Leu Asn Ala Gly
1895 1900 1905

Leu Ile Ser Ala Gly Gly Ser Leu Asp Leu Ser Ala Ile Gly Asp
1910 1915 1920

Ile Ser Asn Ile Ser Ser Val Ile Ser Gly Lys Thr Val Gln Leu
1925 1930 1935

Glu Ser Val Ser Gly Asn Ile Ser Asn Ile Thr Arg Arg Gln Gln
1940 1945 1950

Trp Asn Ala Gly Ser Asp Ser Gln Tyr Gly Gly Val His Leu Ser
1955 1960 1965

Gly Thr Asp Thr Gly Pro Val Ala Thr Ile Lys Gly Thr Asp Ser
1970 1975 1980

Leu Ser Leu Asp Ala Gly Lys Asn Ile Asp Ile Thr Gly Ala Thr
1985 1990 1995

Val Ser Ser Gly Gly Asp Leu Gly Met Ser Ala Gly Asn Asp Ile
2000 2005 2010

```
Asn Ile  Ala Ala Asn Leu Ile  Ser Gly Ser Lys Ser  Gln Ser Gly
    2015                 2020                 2025

Phe Trp  His Thr Asp Asp Asn  Ser Ser Ser Ser Thr  Thr Ser Gln
    2030                 2035                 2040

Gly Ser  Ser Ile Ser Ala Gly  Gly Asn Leu Ala Met  Ala Ala Gly
    2045                 2050                 2055

His Asn  Leu Asp Val Thr Ala  Ser Ser Val Ser Ala  Gly His Ser
    2060                 2065                 2070

Ala Leu  Leu Ser Cys Arg Ser  Arg Pro Ser Leu Glu  Cys Ser Gln
    2075                 2080                 2085

Gly Lys  Ala Lys Thr Ser Arg  Asn Gly Arg Ser Glu  Ser His Glu
    2090                 2095                 2100

Ser His  Ala Ala Val Ser Thr  Val Thr Ala Gly Asp  Asn Phe Leu
    2105                 2110                 2115

Leu Val  Ala Gly Arg Asp Ile  Ala Ser Gln Ala Ala  Gly Met Ala
    2120                 2125                 2130

Ala Glu  Asn Asn Val Val Ile  Arg Gly Gly Arg Asp  Val Asn Leu
    2135                 2140                 2145

Val Ala  Glu Ser Ala Gly Ala  Gly Asp Ser Tyr Thr  Ser Lys Lys
    2150                 2155                 2160

Lys Lys  Glu Ile Asn Glu Thr  Val Arg Gln Gln Gly  Thr Glu Ile
    2165                 2170                 2175

Ala Ser  Gly Gly Asp Thr Thr  Val Asn Ala Gly Arg  Asp Ile Thr
    2180                 2185                 2190

Ala Val  Ala Ser Ser Val Thr  Ala Thr Gly Asn Ile  Ser Val Asn
    2195                 2200                 2205

Ala Gly  Arg Asp Val Ala Leu  Thr Thr Ala Thr Glu  Ser Asp Tyr
    2210                 2215                 2220
```

His Tyr Leu Glu Thr Lys Lys Lys Ser Gly Gly Phe Leu Ser Lys
2225 2230 2235

Lys Thr Thr Arg Thr Ile Ser Glu Asp Ser Ala Thr Arg Glu Ala
2240 2245 2250

Gly Ser Leu Leu Ser Gly Asn Arg Val Thr Val Asn Ala Gly Asp
2255 2260 2265

Asn Leu Thr Val Glu Gly Ser Asp Val Val Ala Asp Arg Asp Val
2270 2275 2280

Ser Leu Ala Ala Gly Asn His Val Asp Val Leu Ala Ala Thr Ser
2285 2290 2295

Thr Asp Thr Ser Trp Arg Phe Lys Glu Thr Lys Lys Ser Gly Leu
2300 2305 2310

Met Gly Thr Gly Gly Ile Gly Phe Thr Ile Gly Ser Ser Lys Thr
2315 2320 2325

Thr His Asp Arg Arg Glu Ala Gly Thr Thr Gln Ser Gln Ser Ala
2330 2335 2340

Ser Thr Ile Gly Ser Thr Ala Gly Asn Val Ser Ile Thr Ala Gly
2345 2350 2355

Lys Gln Ala His Ile Ser Gly Ser Asp Val Ile Ala Asn Arg Asp
2360 2365 2370

Ile Ser Ile Thr Gly Asp Ser Val Val Val Asp Pro Gly His Asp
2375 2380 2385

Arg Arg Thr Val Asp Glu Lys Phe Glu Gln Lys Lys Ser Gly Leu
2390 2395 2400

Thr Val Ala Leu Ser Gly Thr Val Gly Ser Ala Ile Asn Asn Ala
2405 2410 2415

Val Thr Ser Ala Gln Glu Thr Lys Glu Ser Ser Asp Ser Arg Leu
2420 2425 2430

Lys Ala Leu Gln Ala Thr Lys Thr Ala Leu Ser Gly Val Gln Ala
2435 2440 2445

Gly Gln Ala Ala Thr Met Ala Ser Ala Thr Gly Asp Pro Asn Ala
2450 2455 2460

Gly Val Ser Leu Ser Leu Thr Thr Gln Lys Ser Lys Ser Gln Gln
2465 2470 2475

His Ser Glu Ser Asp Thr Val Ser Gly Ser Thr Leu Asn Ala Gly
2480 2485 2490

Asn Asn Leu Ser Val Val Ala Thr Gly Lys Asn Arg Gly Asp Asn
2495 2500 2505

Arg Gly Asp Ile Val Ile Ala Gly Ser Gln Leu Lys Ala Gly Gly
2510 2515 2520

Asn Thr Ser Leu Asp Ala Ala Asn Asp Ile Leu Leu Ser Gly Ala
2525 2530 2535

Ala Asn Thr Gln Lys Thr Thr Gly Arg Asn Ser Ser Ser Gly Gly
2540 2545 2550

Gly Val Gly Val Ser Ile Gly Ala Gly Lys Gly Ala Gly Ile Ser
2555 2560 2565

Ala Phe Ala Ser Val Asn Ala Ala Lys Gly Arg Glu Lys Gly Asn
2570 2575 2580

Gly Thr Thr Thr Asp Lys Thr Val Thr Ile Asn Ser Gly Arg Asp
2585 2590 2595

Thr Val Leu Asn Gly Ala Gln Val Asn Gly Asn Arg Ile Ile Ala
2600 2605 2610

Asp Val Gly His Asp Leu Leu Ile Ser Ser Gln Gln Asp Thr Ser
2615 2620 2625

Lys Tyr Asp Ser Lys Gln Thr Ser Val Ala Ala Gly Gly Ser Phe
2630 2635 2640

Thr Phe Gly Ser Met Thr Gly Ser Gly Tyr Ile Ala Ala Ser Arg

2645 2650 2655

Asp Lys Met Lys Ser Arg Phe Asp Ser Val Ala Glu Gln Thr Gly
2660 2665 2670

Met Phe Ala Arg Val Met Val Ala Ser Thr Ser Gln Trp Val Asn
2675 2680 2685

Ile Pro Asn Trp Met Val Arg Ser Leu Pro His Cys His Thr Gly
2690 2695 2700

Glu Lys Pro Pro Gly Tyr Arg Thr Leu Gly Leu Val Thr Leu Gln
2705 2710 2715

Arg Ser Gly Ile Ile Lys Ser Ser His Arg Trp Asn Gln Ser
2720 2725 2730

<210> 44
<211> 321
<212> PRT
<213> Escherichia coli
<400> 44

Met Met Leu Lys Lys Thr Ile Phe Ile Leu Thr Leu Phe Ser Gly Asn
1 5 10 15

Val Ile Ala Ala Thr Val Glu Leu Gly Phe Glu Asn Glu Gln Tyr Asn
20 25 30

Tyr Ala Tyr Arg Ser Ala Asp Val Phe Met Pro Tyr Ile Lys Ser Asn
35 40 45

Phe Asn Pro Val Thr Asp Ser Ala Leu Asn Val Ser Leu Thr Tyr Met
50 55 60

Tyr Gln Asp Gln Tyr Gly Lys Lys His Lys Lys Thr Ser Glu Asp Arg
65 70 75 80

Phe Lys Thr Asn Arg Asp Arg Ile Glu Leu Tyr Leu Lys Gly Tyr Thr
85 90 95

Leu Asn Arg Gly Ala Tyr Ser Phe Ser Pro Ser Ala Gly Phe Arg Tyr
100 105 110

Glu Ser Trp Asp Val Asn Tyr Asp Asn Pro Lys Lys Gln Asp Lys Trp
115 120 125

Lys Leu Glu Leu Arg Phe Tyr Pro Asn Met Thr Tyr Lys Leu Asn Asp
130 135 140

Gln Leu Ser Leu Tyr Met Asn Gly Phe Val Ala Pro Val Phe Phe Lys
145 150 155 160

Thr Gln Gln Glu Ser Arg Lys Asp Asn Asn Tyr Val Lys Gly Lys Leu
165 170 175

Gly Ala Lys Arg Tyr Asn Asn Asp Tyr Tyr Gln Glu Leu Gln Ile Leu
180 185 190

Gly Val Arg Tyr Lys Phe Asn Asn Asp Asn Thr Leu Trp Ala Ser Val
195 200 205

Tyr Asn Glu Arg Lys Tyr Asn Gln His Ser Ser Lys Tyr Asp Arg Trp
210 215 220

Gln Leu Arg Gly Gly Tyr Asp Phe Lys Val Thr Glu Glu Phe Val Leu
225 230 235 240

Ser Pro Phe Ile Arg Tyr Asp Leu Ser Tyr Arg Glu Lys Asn Leu Glu
245 250 255

Ser Thr Ser Asn Asn Gly Leu Ser Lys Asn Asn Lys Glu Ile Arg Thr
260 265 270

Gly Ala Ser Phe Ser Tyr Lys Ile Ile Pro Ser Val Lys Leu Val Gly
275 280 285

Glu Ile Tyr Arg Gln Thr Thr Asn Ile Glu Asn Tyr Tyr Gly Glu His
290 295 300

Ser Glu Asp Lys Asn Arg Met Phe Tyr Lys Leu Gly Ile Asn Lys Thr
305 310 315 320

Phe

<210> 45

<211> 587
<212> PRT
<213> Escherichia coli
<400> 45

Met Gln His Arg Gln Lys Asn Ile Leu Thr Lys Thr Ser Leu Leu Ser
1 5 10 15

Arg Ala Leu Ser Val Pro Cys Cys Asp Met Phe Arg Arg Gly Ser Pro
20 25 30

Trp Ile Cys Tyr Leu Ser Leu Ser Val Phe Ser Gly Cys Phe Ile Pro
35 40 45

Ala Phe Ser Ser Pro Ala Ala Met Leu Ser Pro Gly Asp Arg Ser Ala
50 55 60

Ile Gln Gln Gln Gln Gln Leu Leu Asp Glu Asn Gln Arg Gln Arg
65 70 75 80

Asp Ala Leu Glu Arg Pro Leu Thr Ile Thr Pro Ser Pro Glu Thr Ser
85 90 95

Ala Gly Thr Glu Gly Pro Cys Phe Thr Val Ser Ser Ile Val Val Ser
100 105 110

Gly Ala Thr Arg Leu Thr Ser Ala Glu Thr Asp Arg Leu Val Pro Trp
115 120 125

Val Asn Gln Cys Leu Asn Ile Thr Gly Leu Thr Ala Val Thr Asp Ala
130 135 140

Val Thr Asp Gly Tyr Ile Arg Arg Gly Tyr Ile Thr Ser Arg Ala Phe
145 150 155 160

Leu Thr Glu Gln Asp Leu Ser Gly Gly Val Leu His Ile Thr Val Met
165 170 175

Glu Gly Arg Leu Gln Gln Ile Arg Ala Glu Gly Ala Asp Leu Pro Ala
180 185 190

Arg Thr Leu Lys Met Val Phe Pro Gly Met Glu Gly Lys Val Leu Asn
195 200 205

Leu Arg Asp Ile Glu Gln Gly Met Glu Gln Ile Asn Arg Leu Arg Thr
210 215 220

Glu Pro Val Gln Ile Glu Ile Ser Pro Gly Asp Arg Glu Gly Trp Ser
225 230 235 240

Val Val Thr Leu Thr Ala Leu Pro Glu Trp Pro Val Thr Gly Ser Val
245 250 255

Gly Ile Asp Asn Ser Gly Gln Lys Ser Thr Gly Thr Gly Gln Leu Asn
260 265 270

Gly Val Leu Ser Phe Asn Asn Pro Leu Gly Leu Ala Asp Asn Trp Phe
275 280 285

Val Ser Gly Gly Arg Ser Ser Asp Phe Ser Val Ser His Asp Ala Arg
290 295 300

Asn Phe Ala Ala Gly Val Ser Leu Pro Tyr Gly Tyr Thr Leu Val Asp
305 310 315 320

Tyr Thr Tyr Ser Trp Ser Asp Tyr Leu Ser Thr Ile Asp Asn Arg Gly
325 330 335

Trp Arg Trp Arg Ser Thr Gly Asp Leu Gln Thr His Arg Leu Gly Leu
340 345 350

Ser His Val Leu Phe Arg Asn Gly Asp Met Lys Thr Ala Leu Thr Gly
355 360 365

Gly Leu Gln His Arg Ile Ile His Asn Tyr Leu Asp Asp Val Leu Leu
370 375 380

Gln Gly Ser Ser Arg Lys Leu Thr Ser Phe Ser Val Gly Leu Asn His
385 390 395 400

Thr His Lys Phe Leu Gly Gly Val Gly Thr Leu Asn Pro Val Phe Thr
405 410 415

Arg Gly Met Pro Trp Phe Gly Ala Glu Ser Asp His Gly Lys Arg Gly
420 425 430

Asp Leu Pro Val Asn Gln Phe Arg Lys Trp Ser Val Ser Ala Ser Phe

435 440 445

Gln Arg Pro Val Thr Asp Arg Val Trp Trp Leu Thr Ser Ala Tyr Ala
450 455 460

Gln Trp Ser Pro Asp Arg Leu His Gly Val Glu Gln Leu Ser Leu Gly
465 470 475 480

Gly Glu Ser Ser Val Arg Gly Phe Lys Asp Gln Tyr Ile Ser Gly Asn
485 490 495

Asn Gly Gly Tyr Leu Arg Asn Glu Leu Ser Trp Ser Leu Phe Ser Leu
500 505 510

Pro Tyr Val Gly Thr Val Arg Ala Val Ala Ala Leu Asp Gly Gly Trp
515 520 525

Leu His Ser Asp Ser Asp Asp Pro Tyr Ser Ser Gly Thr Leu Trp Gly
530 535 540

Ala Ala Ala Gly Leu Ser Thr Thr Ser Gly His Val Ser Gly Ser Phe
545 550 555 560

Thr Ala Gly Leu Pro Leu Val Tyr Pro Asp Trp Leu Ala Pro Asp His
565 570 575

Leu Thr Val Tyr Trp Arg Val Ala Val Ala Phe
580 585

<210> 46
<211> 744
<212> PRT
<213> Escherichia coli
<400> 46

Met Asn Lys His Thr Leu Leu Leu Thr Val Leu Phe Leu Asn Leu Ile
1 5 10 15

Cys Thr Pro Val Phe Ala Gln Asn Trp Gln Val Ala Thr Phe Gly Gln
20 25 30

Ser Thr Asp Leu Asn Phe Ser Ser Leu Ile Asp Ser Ala Lys Ile Gly
35 40 45

```
Arg Asn Asn Ala Trp Leu Ala Gly Asn Asn Asn Phe Leu Glu Ala Gly
    50                  55                  60

Lys Phe Tyr Thr Leu Pro Thr Asp Phe Phe Ile Glu Ser Arg Gly Gly
65                  70                  75                  80

Lys Ile Ala Asn Ser His Asp Gly Met Thr Val Phe Tyr Thr Ile Val
                85                  90                  95

Pro Val Thr Gln Thr Phe Arg Leu Glu Ala Asp Leu Thr Leu Glu Gln
            100                 105                 110

Ile Gly Pro Glu Val Asn Gly Lys Ser Pro Ala Gly Gln Glu Gly Ala
        115                 120                 125

Gly Leu Phe Val Arg Asp Ile Ile Gly Pro Gln Arg Gln Glu Pro Gln
    130                 135                 140

Ser Ala Gly Thr Glu Glu Tyr Pro Gln Ala Ser Asn Ile Leu Met Asn
145                 150                 155                 160

Ala Phe Ile Thr Gln Asn Lys Lys Asn Asp Asn Leu Val Gln Ile Thr
                165                 170                 175

Ser Ile Val Arg Glu Gly Val Ile Lys Thr Trp Gly Asn Glu Gly Ile
            180                 185                 190

Thr Ile Lys Lys Gln Pro Ile Ile Glu Asn Ile Asn Phe Thr Gln Lys
        195                 200                 205

Arg Asn Ile His Met Thr Ile Glu Arg Leu Pro Glu Lys Phe Ile Leu
    210                 215                 220

Thr Ala Phe Asp Thr Asp Arg Lys Glu Asn Gln Ser Trp Gln Phe Ser
225                 230                 235                 240

Asp Tyr Ser Gly Phe Met Asn Gln Leu Asp Asn Asn Ser Leu Ala Ile
                245                 250                 255

Gly Phe Phe Ala Ala Arg Asn Ala Lys Leu Arg Val Lys Asn Ala Ser
            260                 265                 270

Phe Lys Pro Gly Lys Pro Leu Val Asp Tyr Lys Gln Leu Thr Ser Arg
```

275 280 285

Gln Phe Ser Arg Val Arg His Lys Ala Pro Glu Leu Phe Leu Ala Ser
290 295 300

Pro Gln Ser Val Val Arg Asn Ser Thr Thr Leu Gln Phe Leu Ala Asn
305 310 315 320

Gln Ala Gly Ile Val Ser Ile Asp Asn Asp Lys Gln Thr Lys Gln Val
325 330 335

Gln Ala Gly Glu Leu Val Gln Phe Pro Val Thr Leu Gln Lys Lys His
340 345 350

Asn Asp Phe Thr Val Asn Phe Asn Val Asp Gly Asn Ile Ser Lys Lys
355 360 365

Ala Ile Arg Ile Glu Gln Val Lys Ser Asn Leu Thr Asp Pro Tyr Glu
370 375 380

Ile Tyr Val Cys Ser Asp Cys Arg Gln Gly Ala Arg Gly Ser Lys Asn
385 390 395 400

Asp Pro Val Asp Leu Gln Thr Ala Val Lys Phe Val Ala Pro Gly Gly
405 410 415

Asn Ile Tyr Leu Asn Asp Gly Gln Tyr His Gly Ile Thr Leu Asp Arg
420 425 430

Glu Leu Ser Gly Ile Pro Gly Lys Tyr Lys Thr Ile Ser Ala Ile Asn
435 440 445

Pro His Lys Ala Ile Phe Ile Asn Lys Thr Phe Asn Leu Asp Ala Ser
450 455 460

Tyr Trp His Leu Lys Ser Val Val Phe Asp Gly Asn Val Asp Asn Gly
465 470 475 480

Asn Asn Lys Pro Ala Tyr Leu Arg Ile Ala Gly Ser Tyr Asn Ile Ile
485 490 495

Glu His Val Ile Ala Arg Asn Asn Asp Asp Thr Gly Ile Ser Ile Ser
500 505 510

Ala Lys Asp Lys Asn Arg Phe Phe Trp Pro Ala His Asn Leu Val Leu
515 520 525

Asn Ser Asp Ser Tyr Asn Asn Leu Asp Leu Ser Gly Ile Asn Ala Asp
530 535 540

Gly Phe Ala Ala Lys Leu Gly Val Gly Pro Gly Asn Ile Phe Arg Gly
545 550 555 560

Cys Ile Ala His Asn Asn Ala Asp Asp Gly Trp Asp Leu Phe Asn Lys
565 570 575

Ile Glu Asp Gly Pro Asn Ala Ser Val Thr Ile Glu Asn Ser Val Ala
580 585 590

Tyr Glu Asn Gly Leu Pro Tyr Asn Lys Ala Asp Ile Leu Lys Gly Ser
595 600 605

Ile Gly Asn Gly Gly Glu Gly Gln Pro Ser Lys Ser Gln Val Ile Asn
610 615 620

Ser Ile Ala Ile Asn Asn Asn Met Asp Gly Phe Thr Asp Asn Phe Asn
625 630 635 640

Thr Gly Ser Leu Ile Val Arg Asn Asn Ile Ala Met Asn Asn Ala Arg
645 650 655

Tyr Asn Tyr Ile Leu Arg Thr Asn Pro Tyr Lys Phe Pro Ser Ser Ile
660 665 670

Leu Phe Asp Asn Asn Tyr Ser Ile Arg Asp Asp Trp Glu Asn Lys Ile
675 680 685

Lys Asp Phe Leu Gly Asp Thr Val Asn Ser Val Asn Tyr Lys Leu Leu
690 695 700

Val Ser His Glu Thr Gly Pro Val Gln Lys Asp Leu Phe Phe Thr Arg
705 710 715 720

Asp Asp Ser Gly Asn Ile Ile Tyr Pro Asp Phe Phe Leu Asn Ile Ile
725 730 735

Asn Lys Phe Asn Glx Thr Met Pro
740

<210> 47
<211> 136
<212> PRT
<213> Escherichia coli
<400> 47

Met Lys Thr Phe Ile Lys Thr Leu Leu Val Ala Val Thr Ile Leu Phe
1 5 10 15

Ser Val Phe Ala Thr Ala Lys Gln Val Lys Leu Pro Asn Asn Ile Lys
20 25 30

Tyr Val Asn Thr Thr Glu Ala Phe Ser Cys Thr Glu Ile Asp Gly Met
35 40 45

Asn Cys Gln Thr Lys Asn Pro Phe Asn Tyr Lys Asp Asn Ser Tyr Val
50 55 60

Phe Val Leu Glu Arg Gly Gly Ala Trp Cys Tyr Asp Tyr Thr Val Ser
65 70 75 80

Val Leu Asn Leu Lys Thr Gly Lys Ala Gln Met Leu Glu Tyr Lys Asp
85 90 95

Asn Gln Leu Cys Ser Gly Ser Asn Lys Pro Phe Phe Glu Ile Lys Asn
100 105 110

Gly Val Pro Thr Val Gly Val Ile Asp Thr Ser Gly Lys Pro Val Val
115 120 125

Val Ala Leu Asp Lys Leu Lys Thr
130 135

<210> 48
<211> 225
<212> PRT
<213> Escherichia coli
<400> 48

Met Gln Leu Pro Val Lys Leu Leu Met Ser Leu Ile Ser Leu Val Ser
1 5 10 15

Val Ile Ala Arg Ala Gly Lys Tyr Lys Asn Tyr Ile Arg Asp Glu Ile
20 25 30

Lys Tyr Trp Arg Tyr Thr Ser Tyr Lys Gly Gly Glu Phe Pro Glu Gly
35 40 45

Phe Thr Asp Glu Lys Phe Ser Ser Ala Ile Tyr Asn Gly Arg Ile Phe
50 55 60

Thr Met Lys Arg Leu His Thr Leu Met Leu Phe Leu Ala Val Leu Phe
65 70 75 80

Thr Gly Phe Asn Val Glu Ala Ala Ser Val Lys Gln Ala Leu Ser Cys
85 90 95

Asp Pro Asn Ala Arg Ala Glu Gln Pro Gly Ala Cys Pro Thr Thr Tyr
100 105 110

Glu Leu Tyr Glu Gly Asp Ala Ala Tyr Lys Ala Ala Leu Asp Lys Ala
115 120 125

Leu Lys Pro Val Gly Leu Ser Gly Met Phe Gly Lys Gly Gly Tyr Met
130 135 140

Asp Gly Pro Gly Gly Asn Val Thr Pro Val Thr Ile Asn Gly Thr Val
145 150 155 160

Trp Leu Gln Gly Asp Gly Cys Lys Ala Asn Thr Cys Gly Trp Asp Phe
165 170 175

Ile Val Thr Leu Tyr Asn Pro Lys Thr His Glu Val Val Gly Tyr Arg
180 185 190

Tyr Phe Gly Leu Asp Asp Pro Ala Tyr Leu Val Trp Phe Gly Glu Ile
195 200 205

Gly Val His Glu Phe Ala Tyr Leu Val Lys Asn Tyr Val Ala Ala Val
210 215 220

Asn
225

<210> 49

<211> 721
<212> PRT
<213> Escherichia coli
<400> 49

Met Lys Thr Gln Ile Thr Phe Ala Ala Leu Leu Pro Ala Leu Ala Ser
1 5 10 15

Phe Ile Pro Leu His Ala His Ala Ser Ser Thr Ser Glu Asp Glu Met
20 25 30

Ile Val Thr Gly Asn Thr Ala Ala Asp Thr Thr Asp Ser Ala Ala Gly
35 40 45

Ala Gly Phe Lys Thr Asn Asp Ile Asp Val Gly Pro Leu Gly Thr Lys
50 55 60

Ser Trp Ile Glu Thr Pro Tyr Ser Ser Thr Thr Val Thr Lys Glu Met
65 70 75 80

Ile Glu Asn Gln Gln Ala Gln Ser Val Ser Glu Met Leu Lys Tyr Ser
85 90 95

Pro Ser Thr Gln Met Gln Ala Arg Gly Gly Met Asp Val Gly Arg Pro
100 105 110

Gln Ser Arg Gly Met Gln Gly Ser Val Val Ala Asn Ser Arg Leu Asp
115 120 125

Gly Leu Asn Ile Val Ser Thr Thr Ala Phe Pro Val Glu Met Leu Glu
130 135 140

Arg Met Asp Val Leu Asn Ser Leu Thr Gly Ala Leu Tyr Gly Pro Ala
145 150 155 160

Ser Pro Ala Gly Gln Phe Asn Phe Val Ala Lys Arg Pro Thr Glu Glu
165 170 175

Thr Leu Arg Lys Val Thr Leu Gly Tyr Gln Ser Arg Ser Ala Phe Thr
180 185 190

Gly His Ala Asp Leu Gly Gly His Phe Asp Glu Asn Lys Arg Phe Gly
195 200 205

Tyr Arg Val Asn Leu Leu Asp Gln Glu Gly Glu Gly Asn Val Asp Asp
210 215 220

Ser Thr Leu Arg Arg Lys Leu Val Ser Val Ala Leu Asp Trp Asn Ile
225 230 235 240

Gln Pro Gly Thr Gln Leu Gln Leu Asp Ala Ser His Tyr Glu Phe Ile
245 250 255

Gln Lys Gly Tyr Val Gly Ser Phe Asn Tyr Gly Pro Asn Val Lys Leu
260 265 270

Pro Ser Ala Pro Asn Pro Lys Asp Lys Asn Leu Ala Leu Ser Thr Ala
275 280 285

Gly Asn Asp Leu Thr Thr Asp Thr Ile Ser Thr Arg Leu Ile His Tyr
290 295 300

Phe Asn Asp Asp Trp Ser Met Asn Ala Gly Val Gly Trp Gln Gln Ala
305 310 315 320

Asp Arg Ala Met Arg Ser Val Ser Ser Lys Ile Leu Asn Asn Gln Gly
325 330 335

Asp Ile Ser Arg Ser Met Lys Asp Ser Thr Ala Ala Gly Arg Phe Arg
340 345 350

Val Leu Ser Asn Thr Ala Gly Leu Asn Gly His Ile Asp Thr Gly Ser
355 360 365

Ile Gly His Asp Leu Ser Leu Ser Thr Thr Gly Tyr Val Trp Ser Leu
370 375 380

Tyr Ser Ala Lys Gly Thr Gly Ser Ser Tyr Ser Trp Gly Thr Thr Asn
385 390 395 400

Met Tyr His Pro Asp Ala Ile Asp Glu Gln Gly Asp Gly Lys Ile Arg
405 410 415

Thr Gly Gly Pro Arg Tyr Arg Ser Ser Val Asn Thr Gln Gln Ser Val
420 425 430

Thr Leu Gly Asp Thr Val Thr Phe Thr Pro Gln Trp Ser Ala Met Phe

435 440 445

Tyr Leu Ser Gln Ser Trp Leu Gln Thr Lys Asn Tyr Asp Lys His Gly
450 455 460

Asn Gln Thr Asn Gln Val Asp Glu Asn Gly Leu Ser Pro Asn Ala Ala
465 470 475 480

Leu Met Tyr Lys Ile Thr Pro Asn Thr Met Ala Tyr Val Ser Tyr Ala
485 490 495

Asp Ser Leu Glu Gln Gly Gly Thr Ala Pro Thr Asp Glu Ser Val Lys
500 505 510

Asn Ala Gly Gln Thr Leu Asn Pro Tyr Arg Ser Lys Gln Tyr Glu Val
515 520 525

Gly Leu Lys Ser Asp Ile Gly Glu Met Asn Leu Gly Ala Ala Leu Phe
530 535 540

Arg Leu Glu Arg Pro Phe Ala Tyr Leu Asp Thr Asp Asn Val Tyr Lys
545 550 555 560

Glu Gln Gly Asn Gln Val Asn Asn Gly Leu Glu Leu Thr Ala Ala Gly
565 570 575

Asn Val Trp Gln Gly Leu Asn Ile Tyr Ser Gly Val Thr Phe Leu Asp
580 585 590

Pro Lys Leu Lys Asp Thr Ala Asn Ala Ser Thr Ser Asn Lys Gln Val
595 600 605

Val Gly Val Pro Lys Val Gln Ala Asn Leu Leu Ala Glu Tyr Ser Leu
610 615 620

Pro Ser Ile Pro Glu Trp Val Tyr Ser Ala Asn Val His Tyr Thr Gly
625 630 635 640

Lys Arg Ala Ala Asn Asp Thr Asn Thr Ser Tyr Ala Ser Ser Tyr Thr
645 650 655

Thr Trp Asp Leu Gly Thr Arg Tyr Thr Thr Lys Val Ser Asn Val Pro
660 665 670

Thr Thr Phe Arg Val Val Val Asn Asn Val Phe Asp Lys His Tyr Trp
675 680 685

Ala Ser Ile Phe Pro Ser Gly Thr Asp Gly Asp Asn Gly Ser Pro Ser
690 695 700

Ala Phe Ile Gly Gly Gly Arg Glu Val Arg Ala Ser Val Thr Phe Asp
705 710 715 720

Phe

<210> 50
<211> 669
<212> PRT
<213> Escherichia coli
<400> 50

Met Lys Asn Ile Thr Leu Trp Gln Arg Leu Arg Gln Val Ser Ile Ser
1 5 10 15

Thr Ser Leu Arg Cys Ala Phe Leu Met Gly Ala Leu Leu Thr Leu Ile
20 25 30

Val Ser Ser Val Ser Leu Tyr Ser Trp His Glu Gln Ser Ser Gln Ile
35 40 45

Arg Tyr Ser Leu Asp Lys Tyr Phe Pro Arg Ile His Ser Ala Phe Leu
50 55 60

Ile Glu Gly Asn Leu Asn Leu Val Val Asp Gln Leu Asn Glu Phe Leu
65 70 75 80

Gln Ala Pro Asn Thr Thr Val Arg Leu Gln Leu Arg Thr Gln Ile Ile
85 90 95

Gln His Leu Asp Thr Ile Glu Arg Leu Ser Arg Gly Leu Ser Ser Arg
100 105 110

Glu Arg Gln Gln Leu Thr Val Ile Leu Gln Asp Ser Arg Ser Leu Leu
115 120 125

Ser Glu Leu Asp Arg Ala Leu Tyr Asn Met Phe Leu Leu Arg Glu Lys

130 135 140

Val Ser Glu Leu Ser Ala Arg Ile Asp Trp Leu His Asp Asp Phe Thr
145 150 155 160

Thr Glu Leu Asn Ser Leu Val Gln Asp Phe Thr Trp Gln Gln Gly Thr
165 170 175

Leu Leu Asp Gln Ile Ala Ser Arg Gln Gly Asp Thr Ala Gln Tyr Leu
180 185 190

Lys Arg Ser Arg Glu Val Gln Asn Glu Gln Gln Gln Val Tyr Thr Leu
195 200 205

Ala Arg Ile Glu Asn Gln Ile Val Asp Asp Leu Arg Asp Arg Leu Asn
210 215 220

Glu Leu Lys Ser Gly Arg Asp Asp Asp Ile Gln Val Glu Thr His Leu
225 230 235 240

Arg Tyr Phe Glu Asn Leu Lys Lys Thr Ala Asp Glu Asn Ile Arg Met
245 250 255

Leu Asp Asp Trp Pro Gly Thr Ile Thr Leu Arg Gln Thr Ile Asp Glu
260 265 270

Leu Leu Asp Met Gly Ile Val Lys Asn Lys Met Pro Asp Thr Met Arg
275 280 285

Glu Tyr Val Ala Ala Gln Lys Ala Leu Glu Asp Ala Ser Arg Thr Arg
290 295 300

Glu Ala Thr Gln Gly Arg Phe Arg Thr Leu Leu Glu Ala Gln Leu Gly
305 310 315 320

Ser Thr His Gln Gln Met Gln Met Phe Asn Gln Arg Met Glu Gln Ile
325 330 335

Val His Val Ser Gly Gly Leu Ile Leu Val Ala Thr Ala Leu Ala Leu
340 345 350

Leu Leu Ala Trp Val Phe Asn His Tyr Phe Ile Arg Ser Arg Leu Val
355 360 365

Lys Arg Phe Thr Leu Leu Asn Gln Ala Val Val Gln Ile Gly Leu Gly
370 375 380

Gly Thr Glu Thr Thr Ile Pro Val Tyr Gly Asn Asp Glu Leu Gly Arg
385 390 395 400

Ile Ala Gly Leu Leu Arg His Thr Leu Gly Gln Leu Asn Val Gln Lys
405 410 415

Gln Gln Leu Glu Gln Glu Ile Thr Asp Arg Lys Val Ile Glu Ala Asp
420 425 430

Leu Arg Ala Thr Gln Asp Glu Leu Ile Gln Thr Ala Lys Leu Ala Val
435 440 445

Val Gly Gln Thr Met Thr Thr Leu Ala His Glu Ile Asn Gln Pro Leu
450 455 460

Asn Ala Leu Ser Met Tyr Leu Phe Thr Ala Arg Arg Ala Ile Glu Gln
465 470 475 480

Thr Gln Lys Glu Gln Ala Ser Met Met Leu Gly Lys Ala Glu Gly Val
485 490 495

Ile Ser Arg Ile Asp Ala Ile Ile Arg Ser Leu Arg Gln Phe Thr Arg
500 505 510

Arg Ala Glu Leu Glu Thr Ser Leu His Ala Val Asp Leu Ala Gln Met
515 520 525

Phe Ser Ala Ala Trp Glu Leu Leu Ala Met Arg His Arg Ser Leu Gln
530 535 540

Ala Thr Leu Val Leu Pro Gln Gly Thr Ala Thr Val Ser Gly Asp Glu
545 550 555 560

Val Arg Thr Gln Gln Val Leu Val Asn Val Leu Ala Asn Ala Leu Asp
565 570 575

Val Cys Gly Gln Gly Ala Val Ile Thr Val Asn Trp Gln Met Gln Gly
580 585 590

```
Lys Thr Leu Asn Val Phe Ile Gly Asp Asn Gly Pro Gly Trp Pro Glu
        595                 600                 605

Ala Leu Leu Pro Ser Leu Leu Lys Pro Phe Thr Thr Ser Lys Glu Val
    610                 615                 620

Gly Leu Gly Ile Gly Leu Ser Ile Cys Val Ser Leu Met Glu Gln Met
625                 630                 635                 640

Lys Gly Glu Leu Arg Leu Ala Ser Thr Met Thr Arg Asn Ala Cys Val
                645                 650                 655

Val Leu Gln Phe Arg Leu Thr Asp Val Glu Asp Ala Lys
            660                 665
```

<210> 51
<211> 753
<212> PRT
<213> Escherichia coli
<400> 51

```
Met Asn Val Ile Lys Leu Ala Ile Gly Ser Gly Ile Leu Leu Leu Ser
1               5                   10                  15

Cys Gly Ala Tyr Ser Gln Ser Ile Ser Glu Lys Thr Asn Ser Asp Lys
            20                  25                  30

Lys Gly Ala Ala Glu Phe Ser Pro Leu Ser Val Ser Val Gly Lys Thr
        35                  40                  45

Thr Ser Glu Gln Glu Ala Leu Glu Lys Thr Gly Ala Thr Ser Ser Arg
    50                  55                  60

Thr Thr Asp Lys Asn Leu Gln Ser Leu Asp Ala Thr Val Arg Ser Met
65                  70                  75                  80

Pro Gly Thr Tyr Thr Gln Ile Asp Pro Gly Gln Gly Ala Ile Ser Val
                85                  90                  95

Asn Ile Arg Gly Met Ser Gly Phe Gly Arg Val Asn Thr Met Val Asp
            100                 105                 110

Gly Ile Thr Gln Ser Phe Tyr Gly Thr Ser Thr Ser Gly Thr Thr Thr
        115                 120                 125
```

```
His Gly Ser Thr Asn Asn Met Ala Gly Val Leu Ile Asp Pro Asn Leu
    130                 135                 140

Leu Val Ala Val Asp Val Thr Arg Gly Asp Ser Ser Gly Ser Glu Gly
145                 150                 155                 160

Ile Asn Ala Leu Ala Gly Ser Ala Asn Met Arg Thr Ile Gly Val Asp
                165                 170                 175

Asp Val Ile Phe Asn Gly Asn Thr Tyr Gly Leu Arg Ser Arg Phe Ser
            180                 185                 190

Val Gly Ser Asn Gly Leu Gly Arg Ser Gly Met Ile Ala Leu Gly Gly
        195                 200                 205

Lys Ser Asp Ala Phe Thr Asp Thr Gly Ser Ile Gly Val Met Ala Ala
    210                 215                 220

Val Ser Gly Ser Ser Val Tyr Ser Asn Phe Ser Asn Gly Ser Gly Ile
225                 230                 235                 240

Asn Ser Lys Glu Phe Gly Tyr Asp Lys Tyr Met Lys Gln Asn Pro Lys
                245                 250                 255

Ser Gln Leu Tyr Lys Met Asp Ile Arg Pro Asp Glu Phe Asn Ser Phe
            260                 265                 270

Glu Leu Ser Ala Arg Thr Tyr Glu Asn Lys Phe Thr Arg Arg Asp Ile
        275                 280                 285

Thr Ser Asp Asp Tyr Tyr Ile Lys Tyr His Tyr Thr Pro Phe Ser Glu
    290                 295                 300

Leu Ile Asp Phe Asn Val Thr Ala Ser Thr Ser Arg Gly Asn Gln Lys
305                 310                 315                 320

Tyr Arg Asp Gly Ser Leu Tyr Thr Phe Tyr Lys Thr Ser Ala Gln Asn
                325                 330                 335

Arg Ser Asp Ala Leu Asp Ile Asn Asn Thr Ser Arg Phe Thr Val Ala
            340                 345                 350
```

```
Asp Asn Asp Leu Glu Phe Met Leu Gly Ser Lys Leu Met Arg Thr Arg
        355                 360                 365

Tyr Asp Arg Thr Ile His Ser Ala Ala Gly Asp Pro Lys Ala Asn Gln
    370                 375                 380

Glu Ser Ile Glu Asn Asn Pro Phe Ala Pro Ser Gly Gln Gln Asp Ile
385                 390                 395                 400

Ser Ala Leu Tyr Thr Gly Leu Lys Val Thr Arg Gly Ile Trp Glu Ala
                405                 410                 415

Asp Phe Asn Leu Asn Tyr Thr Arg Asn Arg Ile Thr Gly Tyr Lys Pro
            420                 425                 430

Ala Cys Asp Ser Arg Val Ile Cys Val Pro Gln Gly Ser Tyr Asp Ile
        435                 440                 445

Asp Asp Lys Glu Gly Gly Phe Asn Pro Ser Val Gln Leu Ser Ala Gln
    450                 455                 460

Val Thr Pro Trp Leu Gln Pro Phe Ile Gly Tyr Ser Lys Ser Met Arg
465                 470                 475                 480

Ala Pro Asn Ile Gln Glu Met Phe Phe Ser Asn Ser Gly Gly Ala Ser
                485                 490                 495

Met Asn Pro Phe Leu Lys Pro Glu Arg Ala Glu Thr Trp Gln Ala Gly
            500                 505                 510

Phe Asn Ile Asp Thr Arg Asp Leu Leu Val Glu Gln Asp Ala Leu Arg
        515                 520                 525

Phe Lys Ala Leu Ala Tyr Arg Ser Arg Ile Gln Asn Tyr Ile Tyr Ser
    530                 535                 540

Glu Ser Tyr Leu Val Cys Ser Gly Gly Arg Lys Cys Ser Leu Pro Glu
545                 550                 555                 560

Val Ile Gly Asn Gly Trp Glu Gly Ile Ser Asp Glu Tyr Ser Asp Asn
                565                 570                 575
```

Met Tyr Ile Tyr Val Asn Ser Ala Ser Asp Val Ile Ala Lys Gly Phe
580 585 590

Glu Leu Glu Met Asp Tyr Asp Ala Gly Phe Ala Phe Gly Arg Leu Ser
595 600 605

Phe Ser Gln Gln Gln Thr Asp Gln Pro Thr Ser Ile Ala Ser Thr His
610 615 620

Phe Gly Ala Gly Asp Ile Thr Glu Leu Pro Arg Lys Tyr Met Thr Leu
625 630 635 640

Asp Thr Gly Val Arg Phe Phe Asp Asn Ala Leu Thr Leu Gly Thr Ile
645 650 655

Ile Lys Tyr Thr Gly Lys Ala Arg Arg Leu Ser Pro Asp Phe Glu Gln
660 665 670

Asp Glu His Thr Gly Ala Ile Ile Lys Gln Asp Leu Pro Gln Ile Pro
675 680 685

Thr Ile Ile Asp Leu Tyr Gly Thr Tyr Glu Tyr Asn Arg Asn Leu Thr
690 695 700

Leu Lys Leu Ser Val Gln Asn Leu Met Asn Arg Asp Tyr Ser Glu Ala
705 710 715 720

Leu Asn Lys Leu Asn Met Met Pro Gly Leu Gly Asp Glu Thr His Pro
725 730 735

Ala Asn Ser Ala Arg Gly Arg Thr Trp Ile Phe Gly Gly Asp Ile Arg
740 745 750

Phe

<210> 52
<211> 133
<212> PRT
<213> Escherichia coli
<400> 52

Met Ser Ser Lys Thr Lys Cys Trp Leu Trp Met Leu Leu Val Ile Leu
1 5 10 15

Ser Glu Thr Ser Ala Thr Ser Thr Leu Lys Met Phe Asp Asn Ser Glu
20 25 30

Gly Met Thr Lys Thr Leu Leu Leu Ala Leu Ile Val Val Leu Tyr Cys
35 40 45

Ile Cys Tyr Tyr Ser Leu Ser Arg Ala Val Lys Asp Ile Pro Val Gly
50 55 60

Leu Ala Tyr Ala Thr Trp Ser Gly Thr Gly Ile Leu Met Val Ser Thr
65 70 75 80

Leu Gly Ile Leu Phe Tyr Gly Gln His Pro Asp Thr Ala Ala Ile Ile
85 90 95

Gly Met Val Ile Ile Ala Ser Gly Ile Ile Ile Met Asn Leu Phe Ser
100 105 110

Lys Met Gly Ser Glu Glu Ala Glu Glu Thr Pro Val Thr Asn Leu Asp
115 120 125

Lys Lys Ile Ala Asn
130

<210> 53
<211> 286
<212> PRT
<213> Escherichia coli
<400> 53

Met Tyr Ile Lys Lys His Trp Ile Ala Leu Ser Ile Leu Leu Ile Pro
1 5 10 15

Cys Ile Gly Asn Ala Gln Glu Ile Lys Ile Asp Glu Ser Trp Leu His
20 25 30

Gln Ser Leu Asn Val Ile Gly Arg Thr Asp Ser Arg Phe Gly Pro Arg
35 40 45

Leu Thr Asn Asp Leu Tyr Pro Glu Tyr Thr Val Ala Gly Arg Lys Asp
50 55 60

Trp Phe Asp Phe Tyr Gly Tyr Val Asp Leu Pro Lys Phe Phe Gly Val
65 70 75 80

```
Gly Ser His Tyr Asp Val Gly Ile Trp Asp Glu Gly Ser Pro Leu Phe
                85                  90                  95

Thr Glu Ile Glu Pro Arg Phe Ser Ile Asp Lys Leu Thr Gly Leu Asn
            100                 105                 110

Leu Ala Phe Gly Pro Phe Lys Glu Trp Phe Ile Ala Asn Asn Tyr Val
        115                 120                 125

Tyr Asp Met Gly Asp Asn Gln Ser Ser Arg Gln Ser Thr Trp Tyr Met
    130                 135                 140

Gly Leu Gly Thr Asp Ile Asp Thr Gly Leu Pro Ile Lys Leu Ser Ala
145                 150                 155                 160

Asn Ile Tyr Ala Lys Tyr Gln Trp Gln Asn Tyr Gly Ala Ala Asn Glu
                165                 170                 175

Asn Glu Trp Asp Gly Tyr Arg Phe Lys Ile Lys Tyr Ser Ile Pro Leu
            180                 185                 190

Thr Asn Leu Phe Gly Gly Arg Leu Val Tyr Asn Ser Phe Thr Asn Phe
        195                 200                 205

Asp Phe Gly Ser Asp Leu Ala Asp Lys Ser His Asn Asn Lys Arg Thr
    210                 215                 220

Ser Asn Ala Ile Ala Ser Ser His Ile Leu Ser Leu Leu Tyr Glu His
225                 230                 235                 240

Trp Lys Phe Ala Phe Thr Leu Arg Tyr Phe His Asn Gly Gly Gln Trp
                245                 250                 255

Asn Ala Gly Glu Lys Val Asn Phe Gly Asp Gly Pro Phe Glu Leu Lys
            260                 265                 270

Asn Thr Gly Trp Gly Thr Tyr Thr Thr Ile Gly Tyr Gln Phe
        275                 280                 285
```

<210> 54
<211> 172
<212> PRT

<213> Escherichia coli
<400> 54

Met Arg Ile Ala Pro Arg Thr Phe Phe Ala Ile Ser Ala Leu Ala Phe
1 5 10 15

Ile Val Ala Ser Gly Phe Ser Phe Trp Arg Leu Ser Pro Ala Glu Asn
20 25 30

Thr Gly Ile Met Ser Cys Ser Thr Lys Gly Ile Met Arg Phe Glu Asn
35 40 45

Met Glu Lys Glu Asn Val Asn Gly Asn Ile His Phe Asn Phe Gly Ser
50 55 60

Gln Gly Lys Gly Ser Met Val Leu Glu Gly Tyr Thr Asp Ser Ala Ala
65 70 75 80

Gly Trp Leu Tyr Leu Gln Arg Tyr Val Lys Phe Thr Tyr Thr Ser Lys
85 90 95

Arg Val Ser Ala Thr Glu Arg His Tyr Arg Ile Ser Gln Trp Glu Ser
100 105 110

Ser Ala Ser Ser Ile Asp Glu Ser Pro Asp Val Ile Phe Asp Tyr Phe
115 120 125

Met Arg Glu Met Ser Asp Ser His Asp Gly Leu Phe Leu Asn Ala Gln
130 135 140

Lys Leu Asn Asp Lys Ala Ile Leu Leu Ser Ser Ile Asn Ser Pro Leu
145 150 155 160

Trp Ile Cys Thr Leu Lys Ser Gly Ser Lys Leu Asp
165 170

<210> 55
<211> 182
<212> PRT
<213> Escherichia coli
<400> 55

Met Lys Ile Lys Val Ile Ala Leu Ala Thr Phe Val Ser Ala Val Phe
1 5 10 15

```
Ala Gly Ser Ala Met Ala Tyr Asp Gly Thr Ile Thr Phe Thr Gly Lys
            20                  25                  30

Val Val Ala Gln Thr Cys Thr Val Asn Thr Ser Asp Lys Asp Leu Ala
        35                  40                  45

Val Thr Leu Pro Thr Val Ala Thr Ser Ser Leu Lys Asp Asn Ala Ala
    50                  55                  60

Thr Ser Gly Leu Thr Pro Phe Ala Ile Arg Leu Thr Gly Cys Ala Thr
65                  70                  75                  80

Gly Met Asn Ser Ala Gln Asn Val Lys Ala Tyr Phe Glu Pro Ser Ser
                85                  90                  95

Asn Ile Asp Leu Ala Thr His Asn Leu Lys Asn Thr Ala Thr Pro Thr
            100                 105                 110

Lys Ala Asp Asn Val Gln Ile Gln Leu Leu Asn Ser Asn Gly Thr Ser
        115                 120                 125

Thr Ile Leu Leu Gly Glu Ala Asp Asn Gly Gln Asp Val Gln Ser Glu
    130                 135                 140

Thr Ile Gly Ser Asp Gly Ser Ala Thr Leu Arg Tyr Met Ala Gln Tyr
145                 150                 155                 160

Tyr Ala Thr Gly Gln Ser Thr Ala Gly Asp Val Lys Ala Thr Val His
                165                 170                 175

Tyr Thr Ile Ala Tyr Glu
            180
```

<210> 56
<211> 359
<212> PRT
<213> Escherichia coli
<400> 56

```
Met Lys Arg Ile Phe Phe Ile Pro Leu Phe Leu Ile Leu Leu Pro Lys
1               5                   10                  15

Leu Ala Val Ala Gly Pro Asp Asp Tyr Val Pro Ser Gln Ile Ala Val
            20                  25                  30
```

```
Asn Thr Ser Thr Leu Pro Gly Val Val Ile Gly Pro Ala Asp Ala His
        35                  40                  45

Thr Tyr Pro Arg Val Ile Gly Glu Leu Ala Gly Thr Ser Asn Gln Tyr
    50                  55                  60

Val Phe Asn Gly Gly Ala Ile Ala Leu Met Arg Gly Lys Phe Thr Pro
65                  70                  75                  80

Ala Leu Pro Lys Ile Gly Ser Ile Thr Val Tyr Phe Pro Ser Arg Lys
                85                  90                  95

Gln Arg Asp Ser Ser Asp Phe Asp Ile Tyr Asp Ile Gly Val Ser Gly
            100                 105                 110

Leu Gly Ile Ile Ile Gly Met Ala Gly Tyr Trp Pro Ala Thr Pro Leu
        115                 120                 125

Val Pro Ile Asn Ser Ser Gly Ile Tyr Ile Asp Pro Val Gly Ala Asn
    130                 135                 140

Thr Asn Pro Asn Thr Tyr Asn Gly Ala Thr Ala Ser Phe Gly Ala Arg
145                 150                 155                 160

Leu Phe Val Ala Phe Val Ala Thr Gly Arg Leu Pro Asn Gly Tyr Ile
                165                 170                 175

Thr Ile Pro Thr Arg Gln Leu Gly Thr Ile Leu Leu Glu Ala Lys Arg
            180                 185                 190

Thr Ser Leu Asn Asn Lys Gly Leu Thr Ala Pro Val Met Leu Asn Gly
        195                 200                 205

Gly Arg Ile Gln Val Gln Ser Gln Thr Cys Thr Met Gly Gln Lys Asn
    210                 215                 220

Tyr Val Val Pro Leu Asn Thr Val Tyr Gln Ser Gln Phe Thr Ser Leu
225                 230                 235                 240

Tyr Lys Glu Ile Gln Gly Gly Lys Ile Asp Ile His Leu Gln Cys Pro
                245                 250                 255
```

```
Asp Gly Ile Asp Val Tyr Ala Thr Leu Thr Asp Ala Ser Gln Pro Val
            260                 265                 270

Asn Arg Thr Asp Ile Leu Thr Leu Ser Ser Glu Ser Thr Ala Lys Gly
        275                 280                 285

Phe Gly Ile Arg Leu Tyr Lys Asp Ser Asp Val Thr Ala Ile Ser Tyr
    290                 295                 300

Gly Glu Asp Ser Pro Val Lys Gly Asn Gly Ser Gln Trp His Phe Ser
305                 310                 315                 320

Asp Tyr Arg Gly Glu Val Asn Pro His Ile Asn Leu Arg Ala Asn Tyr
                325                 330                 335

Ile Lys Ile Ala Asp Ala Thr Thr Pro Gly Ser Val Lys Ala Ile Ala
            340                 345                 350

Thr Ile Thr Phe Ser Tyr Gln
        355
```

<210> 57
<211> 844
<212> PRT
<213> Escherichia coli
<400> 57

```
Met Asn Ala Asn Asn Leu Ser Cys Leu Ile Tyr Cys Arg Cys Ser Leu
1               5                   10                  15

Leu Leu Phe Ala Ala Leu Gly Leu Thr Val Thr Asn His Ser Phe Ala
            20                  25                  30

Ala Glu Glu Ala Glu Phe Asp Ser Glu Phe Leu His Leu Asp Lys Gly
        35                  40                  45

Ile Asn Ala Ile Asp Ile Arg Arg Phe Ser His Gly Asn Pro Val Pro
    50                  55                  60

Glu Gly Arg Tyr Tyr Ser Asp Ile Tyr Val Asn Asn Val Trp Lys Gly
65                  70                  75                  80

Lys Ala Asp Leu Gln Tyr Leu Arg Thr Ala Asn Thr Gly Ala Pro Thr
                85                  90                  95
```

```
Leu Cys Leu Thr Pro Glu Leu Leu Ser Leu Ile Asp Leu Val Lys Asp
            100                 105                 110

Thr Met Ser Gly Asn Thr Ser Cys Phe Pro Ala Ser Thr Gly Leu Ser
        115                 120                 125

Ser Ala Arg Ile Asn Phe Asp Leu Ser Thr Leu Arg Leu Asn Ile Glu
    130                 135                 140

Ile Pro Gln Ala Leu Leu Asn Thr Arg Pro Arg Gly Tyr Ile Ser Pro
145                 150                 155                 160

Ala Gln Trp Gln Ser Gly Val Pro Ala Ala Phe Ile Asn Tyr Asp Ala
                165                 170                 175

Asn Tyr Tyr Gln Tyr Ser Ser Ser Gly Thr Ser Asn Glu Gln Thr Tyr
            180                 185                 190

Leu Gly Leu Lys Ala Gly Phe Asn Leu Trp Gly Trp Ala Leu Arg His
        195                 200                 205

Arg Gly Ser Glu Ser Trp Asn Asn Ser Tyr Pro Ala Gly Tyr Gln Asn
    210                 215                 220

Ile Glu Thr Ser Ile Met His Asp Leu Ala Pro Leu Arg Ala Gln Phe
225                 230                 235                 240

Thr Leu Gly Asp Phe Tyr Thr Asn Gly Glu Leu Met Asp Ser Leu Ser
                245                 250                 255

Leu Arg Gly Val Arg Leu Ala Ser Asp Glu Arg Met Leu Pro Gly Ser
            260                 265                 270

Leu Arg Gly Tyr Ala Pro Ala Val Arg Gly Ile Ala Asn Ser Asn Ala
        275                 280                 285

Lys Val Thr Ile Tyr Gln Asn Ala His Ile Leu Tyr Glu Thr Thr Val
    290                 295                 300

Pro Ala Gly Pro Phe Val Ile Asn Asp Leu Tyr Pro Ser Gly Tyr Ala
305                 310                 315                 320
```

```
Gly Asp Leu Leu Val Lys Ile Thr Glu Ser Asn Gly Gln Thr Arg Met
                325                 330                 335

Phe Thr Val Pro Phe Ala Ala Val Ala Gln Leu Ile Arg Pro Gly Phe
            340                 345                 350

Ser Arg Trp Gln Met Ser Val Gly Lys Tyr Arg Tyr Ala Asn Lys Thr
        355                 360                 365

Tyr Asn Asp Leu Ile Ala Gln Gly Thr Tyr Gln Tyr Gly Leu Thr Asn
    370                 375                 380

Asp Ile Thr Leu Asn Ser Gly Leu Thr Thr Ala Ser Gly Tyr Thr Ala
385                 390                 395                 400

Gly Leu Ala Gly Leu Ala Phe Asn Thr Pro Leu Gly Ala Ile Ala Ser
                405                 410                 415

Asp Ile Thr Leu Ser Arg Thr Ala Phe Arg Tyr Ser Gly Val Thr Arg
            420                 425                 430

Lys Gly Tyr Ser Leu His Ser Ser Tyr Ser Ile Asn Ile Pro Ala Ser
        435                 440                 445

Asn Thr Asn Ile Thr Leu Ala Ala Tyr Arg Tyr Ser Ser Lys Asp Phe
    450                 455                 460

Tyr His Leu Lys Asp Ala Leu Ser Ala Asn His Asn Ala Phe Ile Asp
465                 470                 475                 480

Asp Val Ser Val Lys Ser Thr Ala Phe Tyr Arg Pro Arg Asn Gln Phe
                485                 490                 495

Gln Ile Ser Ile Asn Gln Glu Leu Gly Glu Lys Trp Gly Gly Met Tyr
            500                 505                 510

Leu Thr Gly Thr Thr Tyr Asn Tyr Trp Gly His Lys Gly Ser Arg Asn
        515                 520                 525

Glu Tyr Gln Ile Gly Tyr Ser Asn Phe Trp Lys Gln Leu Gly Tyr Gln
    530                 535                 540

Ile Gly Leu Ser Gln Ser Arg Asp Asn Glu Gln Gln Arg Arg Asp Asp
```

545 550 555 560

Arg Phe Tyr Ile Asn Phe Thr Leu Pro Leu Gly Gly Ser Val Gln Ser
565 570 575

Pro Val Phe Ser Thr Val Leu Asn Tyr Ser Lys Glu Glu Lys Asn Ser
580 585 590

Ile Gln Thr Ser Ile Ser Gly Thr Gly Gly Glu Asp Asn Gln Phe Ser
595 600 605

Tyr Gly Ile Ser Gly Asn Ser Gln Glu Asn Gly Pro Ser Gly Tyr Ala
610 615 620

Met Asn Gly Gly Tyr Arg Ser Pro Tyr Val Asn Ile Thr Thr Thr Val
625 630 635 640

Gly His Asp Thr Gln Asn Asn Asn Gln Arg Ser Phe Gly Ala Ser Gly
645 650 655

Ala Val Val Ala His Pro Tyr Gly Val Thr Leu Ser Asn Asp Leu Ser
660 665 670

Asp Thr Phe Ala Ile Ile His Ala Glu Gly Ala Gln Gly Ala Val Ile
675 680 685

Asn Asn Ala Ser Gly Ser Arg Leu Asp Phe Trp Gly Asn Gly Val Val
690 695 700

Pro Tyr Val Thr Pro Tyr Glu Lys Asn Gln Ile Ser Ile Asp Pro Ser
705 710 715 720

Asn Leu Asp Leu Asn Val Glu Leu Ser Ala Thr Glu Gln Glu Ile Ile
725 730 735

Pro Arg Ala Asn Ser Ala Thr Leu Val Lys Phe Asp Thr Lys Thr Gly
740 745 750

Arg Ser Leu Leu Phe Asp Ile Arg Met Ser Thr Gly Asn Pro Pro Pro
755 760 765

Met Ala Ser Glu Val Leu Asp Glu His Gly Gln Leu Ala Gly Tyr Val
770 775 780

Ala Gln Ala Gly Lys Val Phe Thr Arg Gly Leu Pro Glu Lys Gly His
785 790 795 800

Leu Ser Val Val Trp Gly Pro Asp Asn Lys Asp Arg Cys Ser Phe Val
805 810 815

Tyr His Val Ala His Asn Lys Asp Asp Met Gln Ser Gln Leu Val Pro
820 825 830

Val Leu Cys Ile Gln His Pro Asn Gln Glu Lys Thr
835 840

<210> 58
<211> 277
<212> PRT
<213> Escherichia coli
<400> 58

Met Val Lys Cys His Thr Leu Ile Asn Arg Arg Asn Lys Cys Leu Leu
1 5 10 15

Ile Val Phe Ile Val Leu Ile Gly Trp Ile Ile Phe Arg Pro Lys Ala
20 25 30

Tyr Thr Tyr Ser Leu Asn Asp Lys Glu Lys Glu Met Leu Ile Met Leu
35 40 45

Ser Gln His Pro Glu Thr Arg Tyr Phe Gly Phe Tyr Ser Ile Glu Leu
50 55 60

Pro Ala Asp Tyr Lys Pro Thr Gly Met Val Met Phe Ile Gln Gly Ser
65 70 75 80

Ala Met Ile Pro Val Glu Thr Lys Leu Gln Tyr Tyr Pro Pro Phe Leu
85 90 95

Gln Tyr Met Thr Arg Tyr Glu Ala Glu Leu Lys Asn Thr Ser Ala Leu
100 105 110

Asp Pro Leu Asp Thr Pro Tyr Leu Lys Gln Val His Pro Leu Ser Pro
115 120 125

Pro Met Asn Gly Val Ile Phe Glu Arg Met Lys Ala Lys Tyr Thr Pro

130 135 140

Asp Phe Ala Arg Val Leu Asp Ala Trp Lys Trp Glu Asn Gly Val Thr
145 150 155 160

Phe Ser Val Lys Ile Glu Ala Lys Asp Gly Arg Ala Thr Arg Tyr Asp
165 170 175

Gly Ile Ser Lys Ile Ala Glu Tyr Ser Tyr Gly Tyr Asn Ile Pro Glu
180 185 190

Lys Lys Val Gln Leu Leu Thr Ile Leu Ser Gly Leu Gln Pro Arg Ala
195 200 205

Asp Asn Gln Pro Pro Ser Glu Asn Lys Leu Ala Ile Gln Tyr Ala Gln
210 215 220

Val Asp Ala Ser Leu Leu Gly Glu Tyr Glu Leu Ser Val Asp Tyr Lys
225 230 235 240

Asn Ser Asn Asn Ile Lys Ile Ser Leu Gln Thr Asp Asn Asn Ser Tyr
245 250 255

Ile Asp Ser Leu Leu Asp Ile Arg Tyr Pro Ser Asn Gly Asn Arg Ala
260 265 270

Trp Tyr Asn Ser Ile
275

<210> 59
<211> 366
<212> PRT
<213> Escherichia coli
<400> 59

Met Leu Pro Glu Pro Val Tyr Arg Arg Trp Ile Ile Leu Leu Ile Ser
1 5 10 15

Met Leu Thr Val Gly Thr Leu Phe Ile Leu Ser Val Trp Asn Ser Ala
20 25 30

Thr Tyr Trp Asp Ile Phe Ile Tyr Gly Val Leu Pro Met Leu Phe Leu
35 40 45

```
Trp Leu Cys Leu Phe Gly Ile Ala Leu Asn Lys Tyr Glu Gln Ser Val
    50                  55                  60

Ala Ala Cys Ile Ser Trp Glu Ser Glu Arg Gln Gln Val Lys Gln Leu
65                  70                  75                  80

Trp Gln His Trp Ser Gln Lys Gln Leu Ala Ile Val Gly Asn Val Leu
                85                  90                  95

Phe Thr Pro Glu Glu Lys Gly Met Ser Val Leu Leu Gly Pro Gln Glu
            100                 105                 110

Glu Ile Pro Ala Tyr Pro Lys Lys Ala Arg Pro Leu Phe Ser Ala Ser
        115                 120                 125

Arg Tyr Ser Leu Ser Ser Ile Phe His Asp Ile His Gln Gln Leu Thr
    130                 135                 140

Gln Gln Phe Pro Asp Tyr Arg His Tyr Leu His Thr Ile Tyr Val Leu
145                 150                 155                 160

Gln Pro Glu Lys Trp Arg Gly Glu Thr Val Arg Gln Ala Ile Phe His
                165                 170                 175

Gln Trp Asp Leu Val Pro Glu Arg Thr Asn Thr Leu Asn Gln Ile Gln
            180                 185                 190

Ser Leu Tyr Asp Glu Arg Phe Asp Gly Leu Ile Leu Val Val Cys Leu
        195                 200                 205

Gln Asn Trp Pro Glu Asn Lys Pro Glu Asp Thr Ser Glu Leu Val Ser
    210                 215                 220

Ala Gln Leu Ile Ser Ser Ser Ser Phe Val Arg Gln His Gln Ile Pro
225                 230                 235                 240

Val Ile Ala Gly Leu Gly Arg Val Met Pro Leu Glu Pro Glu Glu Leu
                245                 250                 255

Glu His Asn Leu Asp Val Leu Phe Glu Tyr Asn Gln Leu Asp Asn Lys
            260                 265                 270

Gln Leu Gln His Val Trp Val Ser Gly Leu Asp Glu Gly Thr Ile Glu
```

275 280 285

Asn Leu Met Gln Tyr Ala Glu Gln His Gln Trp Ser Leu Pro Lys Lys
290 295 300

Arg Pro Leu His Met Ile Asp His Ser Phe Gly Pro Thr Gly Glu Phe
305 310 315 320

Ile Phe Pro Val Ser Leu Ala Met Leu Ser Glu Ala Ala Lys Glu Thr
325 330 335

Glu Gln Asn His Leu Ile Ile Tyr Gln Ser Ala Gln Tyr Ala Gln Lys
340 345 350

Lys Ser Leu Cys Leu Ile Thr Arg Lys Leu Tyr Leu Arg Thr
355 360 365

<210> 60
<211> 260
<212> PRT
<213> Escherichia coli
<400> 60

Met Leu Asn Arg Lys Leu Asn Ile Arg Leu Arg His Ser Leu Asn Ser
1 5 10 15

His Cys Ile Pro Ser Ile Ile Ile Asn Asn Thr Val Arg Ser Phe Gln
20 25 30

Arg Ser Val Met Asn Thr Arg Ala Leu Phe Pro Leu Leu Phe Thr Val
35 40 45

Ala Ser Phe Ser Ala Ser Ala Gly Asn Trp Ala Val Lys Asn Gly Trp
50 55 60

Cys Gln Thr Met Thr Glu Asp Gly Gln Ala Leu Val Met Leu Lys Asn
65 70 75 80

Gly Thr Ile Gly Ile Thr Gly Leu Met Gln Gly Cys Pro Asn Gly Val
85 90 95

Gln Thr Leu Leu Gly Ser Arg Ile Ser Ile Asn Gly Asn Leu Ile Pro
100 105 110

Thr Ser Gln Met Cys Asn Gln Gln Thr Gly Phe Arg Ala Val Glu Val
115 120 125

Glu Ile Gly Gln Ala Pro Glu Met Val Lys Lys Ala Val His Ser Ile
130 135 140

Ala Glu Arg Asp Val Ser Val Leu Gln Ala Phe Gly Val Arg Met Glu
145 150 155 160

Phe Thr Arg Gly Asp Met Leu Lys Val Cys Pro Lys Phe Val Thr Ser
165 170 175

Leu Ala Gly Phe Ser Pro Lys Gln Thr Thr Thr Ile Asn Lys Asp Ser
180 185 190

Val Leu Gln Ala Ala Arg Gln Ala Tyr Ala Arg Glu Tyr Asp Glu Glu
195 200 205

Thr Thr Glu Thr Ala Asp Phe Gly Ser Tyr Glu Val Lys Gly Asn Lys
210 215 220

Val Glu Phe Glu Val Phe Asn Pro Glu Asp Arg Ala Tyr Asp Lys Val
225 230 235 240

Thr Val Thr Val Gly Ala Asp Gly Asn Ala Thr Gly Ala Ser Val Glu
245 250 255

Phe Ile Gly Lys
260

<210> 61
<211> 385
<212> PRT
<213> Escherichia coli
<400> 61

Val Val Ile Ile Asn Ser Thr Ile Leu Ser Gly Ala Gly Ala Ile Pro
1 5 10 15

Ser Leu Thr Ser Leu Leu Pro Asp Ile Arg Lys Met Leu Leu Val Thr
20 25 30

Asp Arg Asn Ile Ala Gln Leu Asp Gly Val Gln Gln Ile Arg Ala Leu
35 40 45

```
Leu Glu Lys His Cys Pro Gln Val Asn Val Ile Asp Asn Val Pro Ala
    50                  55                  60

Glu Pro Thr His His Asp Val Arg Gln Leu Met Asp Ala Pro Gly Asp
65                  70                  75                  80

Ala Ser Phe Asp Val Val Val Gly Ile Gly Gly Gly Ser Val Leu Asp
                85                  90                  95

Val Ala Lys Leu Leu Ser Val Leu Cys His Pro Gln Ser Pro Gly Leu
            100                 105                 110

Asp Ala Leu Leu Ala Gly Glu Lys Pro Thr Gln Arg Val Gln Ser Trp
        115                 120                 125

Leu Ile Pro Thr Thr Ala Gly Thr Gly Ser Glu Ala Thr Pro Asn Ala
    130                 135                 140

Ile Leu Ala Ile Pro Glu Gln Ser Thr Lys Val Gly Ile Ile Ser Gln
145                 150                 155                 160

Val Leu Leu Pro Asp Tyr Val Ala Leu Phe Pro Glu Leu Thr Thr Ser
                165                 170                 175

Met Pro Ala His Ile Ala Ala Ser Thr Gly Ile Asp Ala Leu Cys His
            180                 185                 190

Leu Leu Glu Cys Phe Thr Ala Thr Val Ala Asn Pro Val Ser Asp Asn
        195                 200                 205

Ala Ala Leu Thr Gly Leu Ser Lys Leu Phe Arg His Ile Gln Pro Ala
    210                 215                 220

Val Asn Asp Pro Gln Asp Leu Arg Ala Lys Leu Glu Met Leu Trp Ala
225                 230                 235                 240

Ser Tyr Tyr Gly Gly Val Ala Ile Thr His Ala Gly Thr His Leu Val
                245                 250                 255

His Ala Leu Ser Tyr Pro Leu Gly Gly Lys Tyr His Leu Pro His Gly
            260                 265                 270
```

Val Ala Asn Ala Ile Leu Leu Ala Pro Cys Met Ala Phe Val Arg Pro
275 280 285

Trp Ala Val Glu Lys Phe Ala Arg Val Trp Asp Cys Ile Pro Asp Ala
290 295 300

Glu Thr Ala Leu Ser Ala Glu Glu Lys Ser His Ala Leu Val Thr Trp
305 310 315 320

Leu Gln Ala Leu Val Asn Gln Leu Lys Leu Pro Asn Asn Leu Ala Ala
325 330 335

Leu Gly Val Pro Pro Glu Asp Ile Ala Ser Leu Ser Glu Ala Ala Leu
340 345 350

Asn Val Lys Arg Leu Met Asn Asn Val Pro Cys Gln Ile Asp Leu Gln
355 360 365

Asp Val Gln Ala Ile Tyr Gln Thr Leu Phe Pro Gln His Pro Phe Lys
370 375 380

Glu
385

<210> 62
<211> 105
<212> PRT
<213> Escherichia coli
<400> 62

Met Asn Ile Arg Lys Leu Phe Cys Pro Gly Asn Thr Pro Arg Ile Leu
1 5 10 15

Leu Phe Leu Phe Phe Phe Val Val Ser Ala Ile Thr Thr Ile Ala Cys
20 25 30

Gly Tyr Thr Glu Lys Asn Ala Thr Gly Asn Val Leu Leu Leu Phe Leu
35 40 45

Leu Leu Leu Leu Ala His Arg Asn Thr Leu Thr Ser Ile Thr Ala Leu
50 55 60

Leu Phe Leu Phe Cys Cys Ala Leu Tyr Ala Pro Ala Gly Met Thr Tyr
65 70 75 80

Gly Lys Ile Asn Asn Ser Phe Ile Val Ala Leu Leu Gln Thr Thr Thr
85 90 95

Asp Glu Ala Ala Glu Phe Thr Gly Met
100 105

<210> 63
<211> 147
<212> PRT
<213> Escherichia coli
<400> 63

Met Asn Ile Gln Ala Ile Lys Glu Met Val Asn Leu Ile Cys Ser Phe
1 5 10 15

Leu Phe Ile Phe Phe Leu Ser Ser Ala Phe Val Ser Phe Gly Cys Tyr
20 25 30

Ala Ile Tyr Glu Leu Phe Leu Trp Asn Asp Ile Ile Val Tyr Ser Trp
35 40 45

Gly Tyr Ile Leu Ile Val Phe Leu Pro Phe Thr Leu Tyr Val Met Ser
50 55 60

Phe Glu Ile Leu Phe Phe Ala Ile Ser Gly Arg Arg Leu Ser Lys Val
65 70 75 80

Thr Met Val Arg Leu Trp Leu Ile Ile Lys Ile Ile Ile Ala Phe Ser
85 90 95

Ile Cys Ala Val Leu Ile Phe Ser Ser Ile Tyr Lys Lys Glu Leu Leu
100 105 110

Ser Arg Asn Tyr Ile Ala Cys Ser Gly Ile Pro Ser Gly Trp Met Pro
115 120 125

Gly Leu Ala Thr Lys Tyr Val Lys Glu Lys Ser Leu Cys Glu Lys Asn
130 135 140

Gly Asn Asn
145

<210> 64
<211> 178

<212> PRT
<213> Escherichia coli
<400> 64

Met Phe Pro Ile Arg Phe Lys Arg Pro Ala Leu Leu Cys Met Ala Met
1 5 10 15

Leu Thr Val Val Leu Ser Gly Cys Gly Leu Ile Gln Lys Val Val Asp
20 25 30

Glu Ser Lys Ser Val Ala Ser Ala Val Phe Tyr Lys Gln Ile Lys Ile
35 40 45

Leu His Leu Asp Phe Phe Ser Arg Ser Ala Leu Asn Thr Asp Ala Glu
50 55 60

Asp Thr Pro Leu Ser Thr Met Val His Val Trp Gln Leu Lys Thr Arg
65 70 75 80

Glu Asp Phe Asp Lys Ala Asp Tyr Asp Thr Leu Phe Met Gln Glu Glu
85 90 95

Lys Thr Leu Glu Lys Asp Val Leu Ala Lys His Thr Val Trp Val Lys
100 105 110

Pro Glu Gly Thr Ala Ser Leu Asn Val Pro Leu Asp Lys Glu Thr Gln
115 120 125

Phe Val Ala Ile Ile Gly Gln Phe Tyr His Pro Asp Glu Lys Ser Asp
130 135 140

Ser Trp Arg Leu Val Ile Lys Arg Asp Glu Leu Glu Ala Asp Lys Pro
145 150 155 160

Arg Ser Ile Glu Leu Met Arg Ser Asp Leu Arg Leu Leu Pro Leu Lys
165 170 175

Asp Lys

<210> 65
<211> 209
<212> PRT
<213> Escherichia coli
<400> 65

```
Met Phe Leu Lys Arg Lys Trp Tyr Tyr Ala Val Thr Thr Ser Val Val
1               5                  10                  15

Ile Thr Leu Cys Gly Gly Gly Tyr Tyr Met Tyr Arg Gln Glu Tyr Gln
            20                  25                  30

Met Val Val Thr Val Pro Thr Ala Asp Ala Asn Asp Pro Asn Trp Pro
        35                  40                  45

Asn Lys Arg Ile Gln Phe Asp Thr Ser Glu Trp Leu Gln Gln Leu Gln
    50                  55                  60

Tyr Ile Lys Ile Asp Asp His Tyr Ile Leu Asn Thr Gln Tyr Thr Pro
65                  70                  75                  80

Ile Ala Asn Leu Asp Asp Phe Gly Ile Thr Leu Lys Leu Gln Asn Ala
                85                  90                  95

Leu Asn Gly Ser Asp Lys Arg Leu Pro Ala Leu Tyr Gly Leu Ala Glu
            100                 105                 110

Met Asp Ala Gln Lys Phe Lys Asp Leu Met Arg Gly Lys Ile Lys Cys
        115                 120                 125

Glu Tyr Leu Arg Thr Thr Phe Asp Ala Glu Thr Leu Lys Pro Val Asn
    130                 135                 140

Asp Tyr Phe Leu Ile Ser Phe Thr Tyr Lys Asp Lys Trp Tyr Glu Phe
145                 150                 155                 160

Glu Thr Glu Arg Lys Ile Ser Lys Thr Ser Asp Asp Gly Tyr Phe Leu
                165                 170                 175

Trp Ala Phe Asp Asn Thr Val His Glu Ala Gly Tyr Trp His Asn Thr
            180                 185                 190

Asp Pro Ala Ala Tyr Ser Tyr Arg Asp Tyr Gln Asn Gly Lys Ala Val
        195                 200                 205

Lys
```

<210> 66
<211> 424
<212> PRT
<213> Escherichia coli
<400> 66

Met Asp Ile Trp Arg Gly His Ser Phe Leu Met Thr Ile Ser Ala Arg
1 5 10 15

Phe Arg Gln Tyr Val Phe Ser Leu Met Ser Ile Leu Leu Gln Glu Arg
20 25 30

Lys Met Asn Ile Phe Thr Leu Ser Lys Ala Pro Leu Tyr Leu Leu Ile
35 40 45

Ser Leu Phe Leu Pro Thr Met Ala Met Ala Ile Asp Pro Pro Glu Arg
50 55 60

Glu Leu Ser Arg Phe Ala Leu Lys Thr Asn Tyr Leu Gln Ser Pro Asp
65 70 75 80

Glu Gly Val Tyr Glu Leu Ala Phe Asp Asn Ala Ser Lys Lys Val Phe
85 90 95

Ala Ala Val Thr Asp Arg Val Asn Arg Glu Ala Asn Lys Gly Tyr Leu
100 105 110

Tyr Ser Phe Asn Ser Asp Ser Leu Lys Val Glu Asn Lys Tyr Thr Met
115 120 125

Pro Tyr Arg Ala Phe Ser Leu Ala Ile Asn Gln Asp Lys His Gln Leu
130 135 140

Tyr Ile Gly His Thr Gln Ser Ala Ser Leu Arg Ile Ser Met Phe Asp
145 150 155 160

Thr Pro Thr Gly Lys Leu Val Arg Thr Ser Asp Arg Leu Ser Phe Lys
165 170 175

Ala Ala Asn Ala Ala Asp Ser Arg Phe Glu His Phe Arg His Met Val
180 185 190

Tyr Ser Gln Asp Ser Asp Thr Leu Phe Val Ser Tyr Ser Asn Met Leu
195 200 205

Lys Thr Ala Glu Gly Met Lys Pro Leu His Lys Leu Leu Met Leu Asp
210 215 220

Gly Thr Thr Leu Ala Leu Lys Gly Glu Val Lys Asp Ala Tyr Lys Gly
225 230 235 240

Thr Ala Tyr Gly Leu Thr Met Asp Glu Lys Thr Gln Lys Ile Tyr Val
245 250 255

Gly Gly Arg Asp Tyr Ile Asn Glu Ile Asp Ala Lys Asn Gln Thr Leu
260 265 270

Leu Arg Thr Ile Pro Leu Lys Asp Pro Arg Pro Gln Ile Thr Ser Val
275 280 285

Gln Asn Leu Ala Val Asp Ser Ala Ser Asp Arg Ala Phe Val Val Val
290 295 300

Phe Asp His Asp Asp Arg Ser Gly Thr Lys Asp Gly Leu Tyr Ile Phe
305 310 315 320

Asp Leu Arg Asp Gly Lys Gln Leu Gly Tyr Val His Thr Gly Ala Gly
325 330 335

Ala Asn Ala Val Lys Tyr Asn Pro Lys Tyr Asn Glu Leu Tyr Val Thr
340 345 350

Asn Phe Thr Ser Gly Thr Ile Ser Val Val Asp Ala Thr Lys Tyr Ser
355 360 365

Ile Thr Arg Glu Phe Asn Met Pro Val Tyr Pro Asn Gln Met Val Leu
370 375 380

Ser Asp Asp Met Asp Thr Leu Tyr Ile Gly Ile Lys Glu Gly Phe Asn
385 390 395 400

Arg Asp Trp Asp Pro Asp Val Phe Val Glu Gly Ala Lys Glu Arg Ile
405 410 415

Leu Ser Ile Asp Leu Lys Lys Ser
420

<210> 67
<211> 489
<212> DNA
<213> Escherichia coli
<400> 67
atgaaactga aagctattat attggccacc ggtcttatta actgtattgt attttcagca 60

caggcagtgg atacgacgat tactgtgacg ggtaatgttt tgcaaagaac atgtaatgta 120

ccagggaatg tggatgtttc tttgggtaat ctgtatgtat cagactttcc caatgcagga 180

agtggatctc catgggttaa ttttgatctg tctctcaccg gatgccagaa tatgaatact 240

gttcgggcaa catttagtgg tactgcggat gggcagacat actatgcgaa tacagggaat 300

gctggcggta tcaagattga aattcaggac agggatggaa gtaatgcatc atatcacaat 360

ggtatgttca agacgcttaa tgtacaaaat aataatgcaa cctttaatct taaagcccgt 420

gcagtgagta aaggccaggt tactcctgga aatatcagtt ctgttataac cgtcacctat 480

acctatgcg 489

<210> 68
<211> 2019
<212> DNA
<213> Escherichia coli
<400> 68
atgaaaatga cacggcttta tcctctggcc ttgggggggat tattgctccc cgccattgct 60

aatgcccaga cttcacagca agacgaaagc acgctggtgg ttaccgccag taaacaatct 120

tcccgctcgg catcagccaa caacgtctcg tctactgttg tcagcgcgcc ggaattaagc 180

gacgccggcg tcaccgccag cgacaaactc cccagagtct tgcccgggct caatattgaa 240

aatagcggca acatgctttt ttcgacgatc tcgctacgcg gcgtctcttc agcgcaggac 300

ttctataacc ccgccgtcac cctgtatgtc gatggcgtcc ctcagctttc caccaacacc 360

atccaggcgc ttaccgatgt gcaaagcgtg gagttgctgc gaggcccaca gggaacgtta 420

tatggcaaaa gcgctcaggg cgggatcatc aacatcgtca cccagcagcc ggacagcacg 480

ccgcgcggct atattgaagg cggcgtcagt agccgcgaca gttatcgaag taagttcaac 540

ctgagcggcc ccattcagga tggcctgctg tacggcagcg tcaccctgtt acgccaggtt 600

gatgacggcg acatgattaa ccccgcgacg ggaagcgatg acttaggcgg cacccgcgcc 660

agcataggga atgtgaaact gcgtctggcg ccggacgatc agccctggga aatgggcttt 720

gccgcctcac gcgaatgtac ccgcgccacc caggacgcct atgtgggatg gaatgatatt 780

aagggccgta agctgtcgat cagcgatggt tcaccagacc cgtacatgcg gcgctgcact 840

gacagccaga ccctgagtgg gaaatacacc accgatgact gggttttcaa cctgatcagc 900

gcctggcagc agcagcatta ttcgcgcacc ttcccttccg gttcgttaat cgtcaatatg 960

tctcagcgct ggaatcagga tgtgcaggag ctgcgcgctg caaccctggg cgatgcgcgt 1020

accgttgata tggtgtttgg gctgtaccgg cagaacaccc gcgagaagtt aaattcagcc 1080

tacgacatgc cgacaatgcc ttatttaagc agtaccggct ataccaccgc tgaaacgctg 1140

gccgcataca gtgacctgac ctggcattta accgatcgtt ttgatatcgg cggcggcgtg 1200

cgcttctcgc atgataaatc cagtacacaa tatcacggca gcatgctcgg caacccgttt 1260

ggcgaccagg gtaagagcaa tgacgatcag gtgctcgggc agctatccgc aggctatatg 1320

ctgaccgatg actggagagt gtatacccgt gtagcccagg gatataaacc ttccgggtac 1380

aacatcgtgc ctactgcggg tcttgatgcc aaaccgttcg tcgccgagaa atccatcaac 1440

tatgaacttg gcacccgcta cgaaaccgct gacgtcacgc tgcaagccgc gacgttttat 1500

acccacacca aagacatgca gctttactct ggcccggtcg ggatgcagac attaagcaat 1560

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Seq ID 133

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Seq ID 134

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Seq ID 135

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Seq ID 136

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Seq ID 137

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Seq ID 138

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Seq ID 139

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Seq ID 140

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Seq ID 141

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Seq ID 142

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Seq ID 143

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Seq ID 144

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Seq ID 145

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Seq ID 146

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Seq ID 147

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Seq ID 148

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Seq ID 149

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Seq ID 150

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Seq ID 151

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Seq ID 152

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Seq ID 153

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AAAGGAGCAAGGCTGGAGAACCGTTCCACTCTATTTGCCGACAGTTTCGCTTCTCACTTACTGACATATGGCGGTGAGTA
TTATCGTCAGGAACAACATCCGGGTGGCGCGACGACGGGCTTCCCGCAAGCAAAAATCGATTTTAGCTCTGGTTGGCTAC
AAGATGAGATCACCTTACGCGATCTGCCGATTACCCTGCTTGGCGGAACCCGCTATGACAGTTATCGCGGTAGCAGCGAC
GGCTACAAAGATGTTGATGCCGACAAATGGTCATCTCGTGCGGGGATGACTATCAACCCGACCAACTGGCTGATGTTATT
TGGCTCATATGCTCAGGCATTCCGCGCCCCGACGATGGGCGAAATGTATAACGATTCTAAACACTTCTCGATTGGTCGCT
TCTATACCAACTATTGGGTGCCAAACCCGAACTTACGTCCGGAAACTAACGAAACTCAGGAGTACGGTTTTGGGCTGCGT
TTTGATGACCTGATGTTGTCCAATGATGCTCTGGAATTTAAAGCCAGCTACTTTGATACCAAAGCGAAAGATTATATCTC
CACGACCGTCGATTTCGCGGCGGCGACAACTATGTCGTATAACGTCCCGAACGCCAAAATCTGGGGCTGGGATGTGATGA
CGAAATATACCACTGATCTGTTTAGCCTTGATGTGGCCTATAACCGTACCCGCGGCAAAGACACCGATACCGGGGAATAT
ATCTCCAGCATTAACCCGGATACCGTTACCAGTACCCTGAATATTCCGATCGCTCACAGCGGCTTCTCTGTTGGTTGGGT
CGGTACGTTTGCCGATCGCTCAACACATATCAGCAGCAGCTACAGCAAACAACCTGGCTATGGTGTGAATGATTTCTACG
TCAGTTATCAAGGGCAGCAGGCGCTCAAAGGCATGACCACTACTCTGGTATTGGGCAACGCCTTCGATAAAGAGTACTGG
TCGCCGCAAGGCATCCCACAGGATGGTCGTAACGGAAAAATTTTCGTGAGTTATCAATGG

Seq ID 154

ATGAGGGATGAAATGTTATATAATATACCTTGTCGAATTTATATCCTTTCCACTCTGTCATTATGCATTTCTGGGATAGT
TTCTACTGCAACCGCAACTTCTTCAGAAACAAAAATCAGCAACGAAGAGACGCTCGTCGTGACCACGAATCGTTCGGCAA
GCAACCTTTGGGAAAGCCCGGCGACTATACAGGTTATTGACCAACAAACATTGCAGAACTCCACCAATGCCTCCATAGCC
GATAATTTGCAGGACATCCCCGGAGTAGAGATAACAGACAACTCCTTGGCAGGCCGTAAACAAATCCGCATTCGTGGCGA
AGCATCCTCCCGTGTTTTAATTCTCATTGATGGTCAGGAGGTAACTTATCAGCGCGCCGGAGATAATTATGGTGTGGGAC
TGTTGATAGATGAGTCTGCGCTGGAGCGTGTTGAGGTAGTGAAAGGTCCATATTCCGTACTGTACGGTTCACAGGCAATT
GGCGGTATTGTTAACTTCATAACCAAAAAGGGAGGTGACAAACTTGCATCTGGAGTTGTGAAAGCTGTTTATAATTCCGC
AACAGCAGGCTGGGAAGAATCAATCGCGGTCCAGGGGAGCATCGGTGGATTTGATTATCGCATCAACGGTAGTTATTCTG
ATCAGGGCAATCGTGATACGCCGGATGGACGTCTGCCGAATACCAACTATCGTAACAATAGTCAGGGTGTATGGTTGGGT
TATAACTCCGGAAACCATCGTTTTGGCCTCTCGCTTGATCGCTACAGACTCGCGACGCAAACTTACTATGAGGATCCAGA
CGGAAGCTATGAGGCATTTAGTGTCAAAATACCTAAACTTGAACGAGAGAAAGTTGGGGTATTCTATGACACAGACGTGG
ACGGTGACTATCTAAAAAAAATTCATTTCGACGCGTATGAGCAGACCATCCAGCGCCAATTTGCCAACGAAGTAAAAACG
ACACAGCCTGTTCCCAGTCCGATGATTCAGGCTCTGACCGTTCATAACAAGACTGACACCCATGATAAGCAATACACTCA
GGCGGTCACATTGCAGAGTCACTTTTCGCTGCCTGCTAATAATGAACTTGTTACCGGTGCACAGTACAAACAAGACAGGG
TCAGCCAAAGGTCCGGTGGCATGACCTCAAGCAAATCTCTGACCGGCTTCATTAATAAGGAAACACGAACTCGCTCCTAT
TATGAGTCAGAGCAAAGTACAGTCTCACTATTCGCACAAAATGACTGGCGATTCGCCGATCACTGGACATGGACAATGGG
AGTTCGCCAATACTGGCTTTCTTCAAAGTTGACGCGTGGTGACGGAGTATCATATACCGCAGGCATTATAAGCGATACCT
CTCTTGCCAGAGAGTCTGCGAGTGATCACGAAATGGTAACATCTACAAGCCTGCGCTATTCAGGTTTCGATAACTTGGAG
TTACGCGCTGCGTTCGCGCAAGGCTACGTATTTCCCACACTCTCCCAGCTTTTTATGCAGACATCTGCGGGCGGCAGTGT
CACATACGGAAATCCTGATCTTAAGGCTGAACACTCCAATAACTTTGAATTAGGTGCACGATATAATGGTAATAcGTGGC
TGATTGACAGCGCAGTTTACTACTCAGAAGCTAAAGATTATATTGCAAGTCTGATCTGTGATGGCAGTATAGTTTGCAAT
GGTAACACCAACTCCTCCCGTAGTAGCTACTATTATTATGACAATATTGATCGGGCAAAAACATGGGGACTGGAAATAAG
CGCGGAATATAATGGCTGGGTTTTCTCGCCATATATCAGTGGCAATTTAATTCGTCGGCAATATGAAACTTCAACATTAA
AAACAACTAATACAGGAGAACCAGCGATAAACGGACGTATAGGGCTGAAACATACTCTTGTGATGGGTCAGGCCAACATA
ATCTCTGATGTTTTTATTCGTGCTGCCTCTAGTGCAAAAGATGACAGTAACGGTACCGAAACAAATGTTCCGGGCTGGGC
CACTCTCAACTTTGCAGTAAATACAGAATTCGGTAACGAGGATCAGTCCCGGATTAACCTAGCACTCAATAACCTGACAG
ACAAACGCTACCGTACAGCACATGAAACTATTCCTGCAGCAGGTTTTAATGCAGCTATAGGTTTTGTATGGAATTTC

Seq ID 155

ATGCGTAAAGTTTGTGCAGTCATTTTGTCCGCAGCCATCTGTCT
GTCCGTATCCGGTGCGCCTGCATGGGCGTCTGAACATCAGTCCACACTGAGCGCGGGGTA
TCTTCATGCCCGTACGAACGCTCCCGGCAGCGATAATCTGAACGGGATTAACGTGAAATA
CCGTTATGAGTTTACGGACGCGCTGGGGCTGATTACGTCCTTCAGTTATGCCAATGCTGA
GGATGAGCAAAAAACGCACTACAGCGATACCCGCTGGCATGAAGATTCCGTGCGTAACCG
CTGGTTCAGCGTGATGGCGGGGCCGTCTGTACGCGTGAATGAATGGTTCAGCGCGTATTC
GATGGCGGGTGTGGCTTACAGCCGTGTGTCGACTTTCTCCGGGGATTATCTCCGCGTAAC
TGACAACAAGGGGAAAACGCACGATGTGCTGACCGGAAGTGATGACGGTCGCCACAGCAA
CACGTCTCTGGCGTGGGGGGCTGGCGTGCAGTTTAACCCGACCGAATCCGTGACCATTGA
CCTTGCTTATGAAGGTTCCGGTAGTGGCGACTGGCGAACGGATGCATTTATTGTTGGTAT
CGGATACCGTTTCTGA

Seq ID 156

ATGAAAAAATCGACATTATCTTTAGCCATCGGTTTATTATTGGCATGTAGTACCGGTATGGCAAAAACACAGCATTTAAC
GCTGGAACAACGCCTGGAAGCGGCAGAAATGCGGGCAGCAAAAGCAGAGGGGCAGGTTAAACAGCTTCAGACACAACAAG
CCGCCGAGATCCGCGAAATTAAAACCGCACAGGGCAACACGCCGGTAAACGGTCAATCAACGACGGAGTCAGAGAAGAAA
AACGCCACCCCGCCTAATCTCCTGCTTTCAGGGTATGGCGATTTAAAAATCTACGGTGACGTAGAATTTAATATGGATGC
GGAAAGTAATCATGGCCTGCTGGCAATGACCAACGCTGATGTGAATAGCGATCCCACTAATGAATGGAATCTCAATGGTC
GTATTCTGTTAGGTTTTGATGGTATGCGAAAACTGGATAATGGCTATTTCGCTGGGTTCTCCGCACAACCGCTGGGGGAT
ATGCACGGTTCAGTAAATATCGATGATGCGGTTTTCTTCTTTGGCAAAGAAAACGACTGGAAGGTCAAAGTAGGCCGTTT
TGAAGCCTACGATATGTTCCCGCTGAATCAGGATACCTTTGTTGAACATTCCGGTAATACTGCGAACGATCTTTATGACG
ATGGCAGCGGTTATATCTATATGATGAAAGAGGGCCGCGGACGTTCTAACGCTGGCGGTAATTTCCTCGTCAGCAAACAA
CTCGATAACTGGTATTTTGAATTAAACACGTTACTGGAAGACGGAACATCTTTATATAACGACGGTAATTATCATGGACG
CGATATGGAACAGCAGAAAAATGTTGCTTATCTGCGTCCGGTAATTGCCTGGTCGCCGACGGAAGAATTCACCGTTTCCG
CAGCGATGGAAGCGAATGTGGTAAATAATGCTTATGGTTATACCGATAGCAAGGGTAATTTTGTCGATCAGTCCGATCGT
ACCGGTTATGGCATGAGTATGACCTGGAATGGCCTGAAAACCGATCCGGAAAATGGCATCGTGGTTAATCTTAATACCGC
CTATTTAGATGCTAATAATGAAAAAGATTTCACGGCAGGGATTAACGCGCTGTGGAAACGTTTCGAGCTGGGTTATATCT
ATGCACATAATAAGATTGATGAATTTAGTGGCGTGGTTTGTGATAACGATTGCTGGATTGATGATGAAGGAACATACAAC
ATTCACACCATTCATGCGTCTTATCAGTTCGCTAATGTGATGGATATGGAGAACTTTAATATTTACCTCGGCACGTATTA
CTCCATTCTGGATAGCGACGGCGATAAGATACACGGCGACGATAGTGATGACCGTTACGGCGCACGCGTTCGCTTTAAAT
ACTTCTTC

Seq ID 157

ATGAACGGCAAAGCGTTTCTGGCCTGCGTTCTGATGAGCGTCGTATTAACTGGCTGTGAAACAGCGAAAAAAATCAGCCA
GGTGATCCGCAATCCGGATATTCAGGTCGGAAAGCTGATGGATCAGTCAACCGAGCTGACCGTCACGCTGCTGACCGAGC
CGGACAGCAACCTGACGGCGGATGGCGAAGCCGCGCCGGTGGATGTCCAGTTGGTTTATCTGAGCGACGACTCAAAATTC
CATGCCGCCGACTACGACCAGGTTGCCACCACCGCGCTGCCCGACGTGCTGGGGAAAAACTATATCGATCACCAGGACTT
CAACCTGTTGCCGGATACCGTAAAAACACTGCCGCCGATCAAGTTGGATGAGAAAACCGGTTATATCGGTGTCATTGCCT
ATTTTTCAGACGACCAGGCCACAGAATGGAAACAAATTGAGTCGGTAGAAAGTATCGGCCACCACTATCGCCTGCTGGTG
CATATCCGCGCCAGTGCGATTGAGATGAAAAAAGAGGAAAAC

Seq ID 158

CTGACGCTGGCATGGATTTTTCTGCTGGTGTGGATCTGGTGGCAGGGTCCAAAATGGACGCTCTATGAGCAGCACTGGCT
GGCTCCGCTGGCAAACCGCTGGCTGGCGACCGCCGTCTGGGGACTTATCGCTCTGGTCTGGCTCACCTGGCGGGTGATGA
AGCGTCTGCAAAAGCTGGAAAAACAGCAGAAACAGCAGCGGGAGGAAGAAAAAGATCCGTTGACCGTGGAACTCCACCGC
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GTATATGGTCATTGGTCCTGCGGGTAGCGGCAAAAGCACGCTGCTGCGCGAGGGCTTTCCGTCTGACATTGTTTACACGC
CGGAAAGCATCCGGGGTGTGGAATACCACCCGCTGATCACACCGCGAGTGGGCAACCAGGCGGTAATTTTCGATGTTGAC
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CGTCACATTTACCCGCCGCGCCCATGAAAGTGACGGCTGGCGCAGCGAACTGGGGGCTTTCTGGCAGACGTGGGTACAAC
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CAGATGCAGGGAACAGGAGAAATCGTCACCGCACTGCTCGCCGCATTGCTGGACGGTGAGAACATGGATGTAATGCTGCG
TGGCGTCTGGCTCACATCCTCGCTACAGCGTGGCCAGGTGGATGATATTTTCACGCAGTCCGCCGCCCGCCAGTACGGAC

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CTGGCTGAGCCGAACCTGGCGGGTGAAAACAGCGTCTGGCTGAACAGCTCCCGGCGCAGGCTGACCGCCTTTTCCACCTG
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TGGCACAAGCTAAAGCCTTTATGGACGTACCACCACCGCAGGGAACGGATGAATTCGGCAATCTGCAATTGCCATTGCTT
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CGCCCGCGTAGGGCCGTATGTGGAGCAAACCTACATTCAGCTTCTTGAGCAGCGTTATCTCCCCTCGTTAATGAACGGCC
TGATCCGGGATCTAAACATTGCCCCGCCAGAGAGCGAAGAAAAGCTCGCTGTGCTGCGCGTAGTGCGCATGATGGAAGAC
AAAAGTGGGCGCAACAACGAGGCGGTAAAACAGTACATGGCACGGCGCTGGAGCAATGAATTTCACGGCCAGCGCGATAT
TCAGGCGCAACTGATGGTGCATCTGGACTATGCGCTGGAGCACACCGACTGGCACGCGCAGCGCCAAAGCAGCGACAGCG
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CGTGTCTACCAGACCCTGCGCACCAAAGCATTAAGCGTGTTGCCCGCCGATTTGAATTTGCGCGACCAGGTTGGTCCCAC
CTTCGACAACGTGTTCGTCGCCGGTAATGATGAAAAACTGGTGATCCCGCAGTTCCTCACCCGCTATGGACTGCAAAGCT
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GCGAGGGAAGCGGCGATAAATGAGATGGATTACCGCCTGTTATCCCGGCTGGGGCATGAGTTCGCACCGGAAAACAGCGC
ACTGGAGGAGCAAAAGGACAAGGCGAGTACGCTACAGGCCGTGTACCAGCAACTGACCGAGCTGCACCGTTACCTGCTGG
CGATCCAGAACTCGCCAGTGCCGGGGAAATCGGCGCTGAAAGCAGTACAGCTACGGCTGGATCAAAACAGCAGCGATCCA
ATCTTCGCCACCCGTCAGATGGCAAAAACCCTGCCTGCGCCTCTTAACCGCTGGGTAGGTAAGCTCGCGGATCAGGCCTG
GCATGTGGTGATGGTGGAAGCCGTTCGTTACATGGAAGTGGACTGGCGCGACAATGTAGTGAAACCCTTCAACGAGCAGC
TTGCCGATAACTATCCGTTTAATCCGCGCGCCACACAGGATGCCTCACTGGATTCGTTTGAACGTTTCTTTAAACCGGAT
GGCATTCTGGACAATTTCTACAAGAACAACCTGCGCCTGTTCCTTGAAAACGATCTGACCTTTGGCGACGACGGCAGAGT
GTTAATCCGTGAAGATATCCGGCAGCAACTGGATACCGCGCAGAAAATCCGCGACATCTTCTTCAGCCAGCAGAACGGGC
TGGGCGCACAGTTTGCCGTGGAAACCGTATCGCTTTCCGGCAATAAGCGGCGCAGCGTACTTAACCTGGACGGCCAGTTA
GTGGACTACAGCCAGGGACGCAACTACACCGCCCATCTGGTCTGGCCGAACAACATGCGTGAAGGCAATGAAAGCAAGCT
GACGCTGATTGGCACCAGCGGCAGAGCACCGCGCAGTATCGCGTTCAGTGGACCGTGGGCGCAGTTCCGCCTGTTCGGCG
CGGGCCAGTTGACCAATGTGACCAGTGACACCTTTAACGTGCGCTTTAACGTGGACGGCGGCGCAATGGTTTACCAGGTG
CATGTGGATACCGAAGATAACCCGTTCACCGGCGGTCTGTTCAGCCTGTTCCGTTTACCGGATACGTTGTAT

INTERNATIONAL SEARCH REPORT

International Application No
PCT/EP 03/02925

A. CLASSIFICATION OF SUBJECT MATTER
IPC 7 C12N15/31 C12N15/63 C07K14/245 C07K16/12 A61K39/108
G01N33/53

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 7 C12N C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)
EPO-Internal, WPI Data, PAJ, BIOSIS, CHEM ABS Data, EMBASE

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 01 66572 A (INST NAT SANTE RECH MED ;NASSIF XAVIER (FR); TINSLEY COLIN (FR); B) 13 September 2001 (2001-09-13) SEQ ID NOs:390 and 391 page 3, line 20 - page 4, line 17 page 29, line 23 - line 31	1-6, 9-13,15, 16
A	JOHNSON JAMES R ET AL: "Phylogenetic and pathotypic similarities between Escherichia coli isolates from urinary tract infections in dogs and extraintestinal infections in humans." JOURNAL OF INFECTIOUS DISEASES, vol. 183, no. 6, 2001, pages 897-906, XP002211433 ISSN: 0022-1899 abstract	

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[X] Further documents are listed in the continuation of box C.

[X] Patent family members are listed in annex.

* Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
11 August 2003	05. 12. 2003

Name and mailing address of the ISA	Authorized officer
European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax: (+31-70) 340-3016	Mata-Vicente, M.

INTERNATIONAL SEARCH REPORT

International Application No
PCT/EP 03/02925

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	MUEHLDORFER I ET AL: "Characterization of Escherichia coli strains isolated from environmental water habitats and from stool samples of healthy volunteers." RESEARCH IN MICROBIOLOGY, vol. 147, no. 8, 1996, pages 625-635, XP002211434 ISSN: 0923-2508 table I page 630, paragraph 2	

INTERNATIONAL SEARCH REPORT

International application No.
PCT/EP 03/02925

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. [X] Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

see FURTHER INFORMATION sheet PCT/ISA/210

2. [X] Claims Nos.: 14
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:

see FURTHER INFORMATION sheet PCT/ISA/210

3. [ ] Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. [ ] As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.

2. [ ] As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. [ ] As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:

4. [X] No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-6, 9-13, 15 and 16 partially

Remark on Protest

[ ] The additional search fees were accompanied by the applicant's protest.

[ ] No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Continuation of Box I.1

As far as an "in vivo" method is concerned, claim 9 is directed to a method of treatment of the human/animal body and the search has been carried out and based on the alleged effects of the compound/composition.

As far as an "in vivo" method is concerned, claim 15 is directed to a diagnostic method practised on the human/animal body and the search has been carried out and based on the alleged effects of the compound/composition.

Continuation of Box I.2

Claims Nos.: 14

Claim 14 refers to "monoclonal antibodies against epitopes of polypeptide", but it does not say which polypeptide is meant. In consequence, the scope of said claim is ambiguous and vague and its subject-matter is not sufficiently disclosed and supported (Art. 83 and 84 EPC). Therefore, no search has been carried out on said claim.

The phrase "polypeptide such as used according to claim 9" comprised in Claim 13 lacks any sense. Nevertheless, the ISA has assumed that it is an error and that it refers to the polypeptides referred to in Claim 9 or, in other words, a polypeptide selected from the group comprising SEQ ID NOs:1-66 (except SEQ ID NO:8) and 133-145.

The applicant's attention is drawn to the fact that claims relating to inventions in respect of which no international search report has been established need not be the subject of an international preliminary examination (Rule 66.1(e) PCT). The applicant is advised that the EPO policy when acting as an International Preliminary Examining Authority is normally not to carry out a preliminary examination on matter which has not been searched. This is the case irrespective of whether or not the claims are amended following receipt of the search report or during any Chapter II procedure. If the application proceeds into the regional phase before the EPO, the applicant is reminded that a search may be carried out during examination before the EPO (see EPO Guideline C-VI, 8.5), should the problems which led to the Article 17(2) declaration be overcome.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

Invention 1: Claims (1-6, 9-13, 15 and 16) - partially

Isolated antigenic polypeptide SEQ ID NO:14; the polynucleotide encoding it (SEQ ID NO:80); vector comprising said polynucleotide and host cell transformed with it; antibodies against said polypeptide; vaccines comprising the polypeptide; methods of diagnosis/treatment derived of the use of any of the molecules previously mentioned.

Inventions 2-32: Claims (1-6, 9-13, 15 and 16) - partially

Idem as invention 1, but restricted to each one of the polypeptides of SEQ ID NOs: 15, 17, 21-23, 28-30, 32, 36, 38, 39, 41-44, 46, 49, 50, 52-55, 58, 60, 63 and 133-138 and their corresponding genes (SEQ ID NOs:81, 83, 87-89, 94-96, 98, 102, 104, 105, 107-110, 112, 115, 116, 118, 119 and 126).

Invention 33: Claims (4-6) - partially

Isolated polynucleotide SEQ ID NO:127, vector comprising it and host cell transformed therewith.

Inventions 34-41: Claims (9-13, 15 and 16) - partially

Idem as invention 33, but restricted to each one of the polynucleotides SEQ ID NOs: 130, 132 and 146-151.

Invention 42: Claims (9-13, 15 and 16) - partially

Use of the polypeptide SEQ ID NO:1 as antigen; vaccines; antibodies against said polypeptide; methods of diagnosis/treatment derived of the use thereof.

Inventions 43-86: Claims (9-13, 15 and 16) - partially

Idem as invention 42, but restricted to each one of the polypeptides SEQ ID NOs: 2-7, 9-13, 16, 18-20, 24-27, 31, 33-35, 37, 40, 45, 47, 48, 51, 56, 57, 59, 61, 62, 64-66, 139-145.

Invention 87: Claims (7 and 8) - completely

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Process for isolating and identifying polypeptides useful as vaccines comprising the steps of: selecting on the basis of sequence analysis those of the polypeptides which are either located in the outermembrane or secreted by the bacteria; identifying the genes coding for said polypeptides which are conserved in B2/D clinical isolates; purifying the polypeptides identified in step 1, which are found in step 2 to be conserved in B2/D isolates; and testing the polypeptides for immunogenicity using animal models.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No
PCT/EP 03/02925

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 0166572 A	13-09-2001	FR 2806096 A1	14-09-2001
		CA 2402602 A1	13-09-2001
		WO 0166572 A2	13-09-2001
		EP 1328641 A2	23-07-2003
		US 2003148324 A1	07-08-2003